

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene  
homolog 1 (YES1) gene.

&lt;400&gt; 304

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198/292

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&lt;210&gt; 305

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(459)

<223> 3' terminal sequence. interferon -induced  
protein 75, 52kd (IFI75) gene.

&lt;400&gt; 305

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ncttgctga aggtgtgctg gacacctctt ggggtctctt tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggctctt 120
ctttatctct tatttggggg atcaggttgt cactggccac ttgcacagtg ctagtgagga 180
ggctgggcac ctctctgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
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gggctggcgc actcaactcag gatctcatcg ctttgcctgg agg atgttcc agggctcact 360
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gcncaatngg gtatggaagg aagcttcctt ctaanaagg 459

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&lt;210&gt; 306

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

<221> misc\_feature  
 <222> (1)..(370)  
 <223> 5' terminal sequence. interferon -induced  
 protein 75, 52kd (IFI75) gene.

```
<400> 306
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aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttaccacatga caagagccat ggaagaggct ctttttcagc acttcacga 180
ccagaagctg gggatcgccat atgccataca caagccattt ccttctcttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagatggt tgcacaacat tctcacccaa ctgggagagg actttttaac 360
ctgtncctct 370
```

<210> 307  
 <211> 1541  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1541)  
 <223> interferon-induced protein 75, 52kd (IFI75)  
 gene.

```
<400> 307
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tccaggaaag aagaagcact tcagtgaaca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcactagcac tgtgcaagtg gccagtga 240
acctgatccc ccaataaaga gataaagaag accctcaaga gatgccccac tctcctcttg 300
gctctatcgc agagataaaga gataattctc cagaacccaa t gacccagaa gagccccagg 360
agggtgtccag cacaccttca gacaaagaa gaaagaaaag aaaaagatgt atctggtcaa 420
ctccaaaaag gagacataag aaaaaaagcc tcccaagagg gacagctca tctagacag 480
gaatccaaaa gaagctcaaa aggggtggatc aggttctctc aaagaaagat gactcaactt 540
gttaactccac ggtagagaca agggcccaaa aggcgagaac tgaatgtgcc cgaagtcga 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaagaggg tccagaaga 660
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aaaaaagaaa ggagaagat atctgttcaa gctcaaaaag gagatttcag aaaaatttc 900
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attaatatt cgagattacg gtgagccttt caggaagcaa tgtggttgga cctggttaag 1500
ggaaaggctg attacggaaa tgtcacgggt ggcccggaat t 1541
```

<210> 308  
 <211> 416  
 <212> DNA

200/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(416)

&lt;223&gt; 3' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 308

```

gttannnnan tnnatttttt aagagagagg caatttttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccttgccca catcccccac cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcgag acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctgggtggcag aagggtccct gcaggaggtt cacctgaatg actctcagat tcacagacct 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416

```

&lt;210&gt; 309

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(426)

&lt;223&gt; 5' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 309

```

gaactcatca tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggaccattt caagaaagtc cggaaagtctc tggctcttga catttgtgat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc ccttcaaaact 180
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cgggac

```

&lt;210&gt; 310

&lt;211&gt; 2627

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene  
homolog-like 2 (MYBL2) gene.

```

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gcctcatctc  caacctctc  taggatggg  gatgtggcca  ggggtgtctc  tgtgtcacc  2580
ctctcttgg  gcatTTTTT  ggaagaataa  aatgctctct  cctcttg  2627

```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth factor, beta receptor iii (betaglyc an, 300kd)

(TGFB<sub>3</sub>) gene.

```

<400> 311
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taagcatcc tctctgtctaa ttgacacctt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcacct 240
gacaagtgtt aaggcaacat tcttttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgttttctt ccatacttg catacaccac tggcaaatg tcttaatggc 360
aaattttgta ttctttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggcccatt tc                                     442

```

```

<210> 312
<211> 315
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(315)
<223> 5' terminal sequence. transforming growth
        factor, beta receptor iii (betaglycan, 300kd)
        (TGFB3) gene.

```

```

<400> 312
taacaaggag gtatcactga gcttatattta gctgcaaagt ggcacatatt tattccattt 60
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gagaagtaag gcaatccaaa tgagtgcctt ttccaactct cagcactgtc ttgngngaatt 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcattct 240
gtcagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta                                     315

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```

<210> 313
<211> 4208
<212> DNA/RNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(4208)
<223> transforming growth factor, beta receptor
        iii (betaglycan, 300kd) (TGFB3) gene.

```

```

<400> 313
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4208

<210> 314  
<211> 468  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(468)  
<223> 3' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

<400> 314  
tnntttttttt tttncacctt tccctaatac ttnatnggtn acctetaggc ctgtgtgctgg 60  
ctgggtggggc ttggggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120  
ttgctaggc cctccagggt cccatactgt ggagtttga ggggcaggtc tggcctttcc 180  
tgggtcagca tagggcacc cagggtgggn acaggtggac acccagcaca ggcacctagg 240  
caggggcaca agctcantat ccttagcca gcctaattgt ntttgg agaa atattccttg 300  
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tccagccagc gggacaaant 360  
ttcccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatcccacg 420  
gagngtccca aaggnaaatc attaaacagt gatattggcn aaggaaaa 468

<210> 315  
<211> 394  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(394)  
<223> 5' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

<400> 315  
acttcaaggc cacagcgggt gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60  
aagggaagta cgtggtctctc tttttctacc ctctggactt cactttttgt tgccccaccg 120  
agtcacgcg gttcagcaac cgtgcagagg acttcgcgaa gctgggctgt gaagtgtctg 180  
gcgtctcggg tggaacttca gttcaccac cttgcttga tcaacacccc ccggaagag 240  
ggaggcttgg gccccctgaa cacc cccctg ctgtctgacg tgaccagacg cttgtctgag 300  
gattacggcg tgctgaaaac agatgagggc attgctaaca gggccctctt tatcatcgat 360  
gggcaagggt gttcctttcg ccagatcaat gttta 394

<210> 316  
<211> 937  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>



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<221> misc\_feature  
<222> (1)..(937)  
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316  
cgcgggcccca gggctcactt ggcgctgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60  
tctagcctttt gccacgcag ctttcagtc tggcctccgg taacgcg cgc atcggaagagc 120  
cagccctcga cttcaaggcc acagcgggtg ttgatggcgc cttcaaaagag gtgaagctgt 180  
cggaactaca agggaaagtac gtggtcctct tttctaccc ctgggacttc acttttgtgt 240  
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300  
aagtgtctgg cgtctcggtg gactc tcagt tcacccacct ggcttggtat aacaccccc 360  
ggaaagaggg aggcctgggc ccttgaaca tccocctgct tgctgacgtg accagacgct 420  
tgtctgagga ttacggcggtg ctgaaaaacg atgagggtat tgcttacagg gccctcttta 480  
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ccgtggatga ggctctcgcg ctggtccagg cctccagta cacagacgag catgggggag 600  
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acacaggcct agaggtaac aataaagtat tagggcc 937

<210> 317  
<211> 451  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(451)  
<223> 5' terminal sequence. v-fos fbj murine  
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317  
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atgcagcaga ctgggagcct ctgcacagt gctccctggg gatggggccc atggcacagn 180  
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cttcctctgt cttcacctac ccagagctg actncttccc cagctgtgca ctgccccacc 300  
gcaaggcagc agcagcaatg agccttctc tgaactgttc agctnaccca cgggtgctggc 360  
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420  
tngttgattt anagagagga gaaacaaatt t 451

<210> 318  
<211> 2084  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2084)  
<223> v-fos fbj murine osteosarcoma viral oncogene  
homolog (FOS) gene.

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<400> 318
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ctcggccctc cgcccggtt tgcttaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgaggc gtcate ctcc cgetgcagca ggcggtcccc ggcgggggat agcctctctt 240
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tgtgcacgga cctggccgtc tcagtgcca acttcatctc caccgtcact gccatctcga 360
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agaccagagc cctccaccct ttcgagtc cgcgcctcct cgetggggct tactccaggg 480
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tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaagggaa aggaataaga 600
tggtctgcag caaatgccgc aacggaggga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
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<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding protein 7 (RBBP7) gene.

<400> 319

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ctgcaagcc aatcaagaag tgttggagg aaaaagtgt aagttattc ttgcatattt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaaggcaa 120
taccctgcta cttgtattta aatcaatg tgatgttatt tcttangcaa cattctcttc 180
ttccctaata gctacaant gatacagtc gaacagctc acttgaaagt gctagantca 240

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<210> 320

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<211> 457  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(457)  
 <223> 5' terminal sequence. retinoblastoma -binding  
 protein 7 (RBBP7) gene.

<400> 320  
 agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60  
 agaatacacc gtttctatat gacctggtta tgaccocatg ttttcagtggtg cccagtcctta 120  
 ccgttcagtg gtttctgtaa gtgactaaac ctgaaggaaa agattatggtc cttcattggc 180  
 tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 240  
 ttcccaatga tgatgcacag ttgat gctt cccattgtga cagtgacaag ggtgaatttg 300  
 gtggctttgg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaaggga 360  
 gaagttaaac cgtgctcgtt aacatggcgc cagantcctt cacatccatt gcttacaaan 420  
 acacctctt gottgatggt gttggnnttt tgactat 457

<210> 321  
 <211> 1946  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1946)  
 <223> retinoblastoma -binding protein 7 (RBBP7)  
 gene.

<400> 321  
 gcctcgtcag ctgcctgggc gggc tgggag gcgcgggttg aaaagtctcg ttccaagttt 60  
 ggagagagag agaagagcgc ctacacctc ggtaccgcgc agcggggagg aggcaggaaa 120  
 gaaggacgcg gcgtctgggg agcaccacag cagcaagacg gggcccgggc tticgacagt 180  
 ggggagtggt acgcgcttgg gaaaggcagg agcgcacagc gtcgggctgc ttttgctaa 240  
 cgagaggagt ccgaggcggc ggcgaggggc gaacgaccgc acgcaagatg gcgagtaaa 300  
 agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataataa atctggaaga 360  
 agaatacacc gtttctatat gacctggtta tgaccatgct tcttcagtggt cccagtcctta 420  
 ccgttcagtg gtttctgtaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480  
 tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 540  
 ttcccaatga tgatgcacag ttgatgctt cccattgtga cagtgacaag ggtgaatttg 600  
 gtggctttgg ttctgtaaca ggaanaattg aatgtgaaat taaaatcaat cacgaaggag 660  
 aagttaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaacaccatt 720  
 cttctgatgt gttggttttt gactatacaa aacacctcgc taaaccagac ccaagtggag 780  
 aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggcgatggt ctctcctgga 840  
 attcaaatat gaggggacat ctctctaagt catctgatga ccatactggt tgtctgtggg 900  
 atataaacgc aggaacaaaa gaaggcaaaa ttgtggatgc taaagccatc ttactctggc 960  
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atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
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agccttgggt cattttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtccagatg tcacgacatc cgaactggag ggaca aggat 1560
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gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaaat

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&lt;210&gt; 322

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 322

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tatagaaatt ctttattatt agacaaaaat agactctctt ttttccccta ttcattgtat 60
cctactctga atctctgctc agaggaggca gtgactcgtc ccccaccctc ctcccattccc 120
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&lt;210&gt; 323

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 323

```

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209/292

<210> 324  
 <211> 489  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(489)  
 <223> 5' terminal sequence. atp-binding cassette,  
 sub-family c (cftr/mrp), member 5 (ABCC5) gene.

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 actgtgatga agtgatcttc atgaaagagg gctgtatita cgggaagagg ggacacctg 360  
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 ttcacagtt 489

<210> 325  
 <211> 5838  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(5838)  
 <223> atp-binding cassette, sub-family c  
 (cftr/mrp), member 5 (ABCC5) gene.

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<210> 326  
 <211> 385  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(385)  
 <223> 3' terminal sequence. cadherin 1, type 1,  
 e-cadherin (epithelial) (CDH1) gene.

```

<400> 326
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<210> 327  
 <211> 423  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(423)  
 <223> 5' terminal sequence. cadherin 1, type 1,  
 e-cadherin (epithelial) (CDH1) gene.

```

<400> 327
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ggcttccctc ttctctctcc tgagtatgta acttgcaatg ggacgtatc c agtgacttg 180

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ggg                                         423

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&lt;210&gt; 328

&lt;211&gt; 4828

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)  
(CDH1) gene.

&lt;400&gt; 328

```

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tagtgcttaa agtgcgtcag ccaagacagc agcggaacta tgaagagtg gcttgagat 4140
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gtgggtctac ctcatctctg aaaattcttg aaggaatgga ggagtctcaa catgtgttc 4260
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aaaccgagaa tattcaaaat tccaaaatttt ttcttaggag caagaagaaa atgtggccct 4440
aaagggggtt agttgagggg tagggggtag tgaggatctt gatttggatc tctttttatt 4500
taaatgtgaa tttcaacttt tgacaatcaa agaaaagact tttgttgaaa tagctttact 4560
gtttctcaag tgttttgagg aaaaaatca accctgcaat cacttttttg aattgtcttg 4620
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tttagtgtat acatgtgtgg gtgctgataa ttgtgtattt tctttggggg tggaaaaagg 4740
aaacaattca agctgagaaa agtatctca aagatgcatt tttataaatt ttattaaaca 4800
attttgttaa accataaaaa aaaaaaaa 4828

```

&lt;210&gt; 329

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(471)

<223> 5' terminal sequence. zinc finger protein  
144 (mel-18) (ZNF144) gene.

&lt;400&gt; 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tcccagctcc cccccc cc 60
gaccccgcaa tcatgcacg gactacacgg atcaaaatca cagagctgaa ccccccactc 120

```

214/292

```

atgtgtgcc  tctgcgggg  gtacttcac  gacgccacca  ctatcgtgga  gtgcctgcac  180
tcctttcgca  aaacctgcat  cgtgcgtac  ctggagacca  acaataactg  ccccatgtgt  240
gacgtgcagg  tccataaaac  ccggccgctg  ctgagca  ttc  aggtctgaca  aaacatttca  300
agacattgtc  ttacaatttg  gtccctgggg  ctttttaaa  atggagattg  aaacggggcg  360
cgggatttct  tatggcaggc  gttacccttt  ggacgggagg  tcccccaac  ggnttccaat  420
tgagggacgc  ngggcgaggg  ttttnggga  ggcagggaga  aggggggttt  t  471

```

&lt;210&gt; 330

&lt;211&gt; 2227

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)  
gene.

&lt;400&gt; 330

```

gagagccgca  acaggaagag  ggtacagctt  tgtg caggtc  acatgccacc  tgcagccctc  60
cagccctctg  tccccagagc  ggacttttga  agctgaactg  cttttgttgc  tggaaagact  120
atgttataat  ttacctggg  tggaccaggg  tcgtacaaaa  gggcaacgct  ccccgctccc  180
cccactcccg  accccgggat  catgcctcgg  actacaagg  tcaaaatcac  agagctgaac  240
ccccacctca  tgt gtgccct  ctgcgggggg  tacttcacgc  acgcccacc  tatcgtggag  300
tgccctgcat  ccttctgcaa  aaacctgcac  gtgcgtacc  tggagaccac  caaataactg  360
cccatgtgtg  acgtgcagg  ccataaaacc  ogcccgctgc  tgagcatcag  gtctgacaaa  420
acactccaag  acattgtcta  caaattggct  cctggccttt  ttaagatga  gatga aacgg  480
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tcggcgaggg  tcttggagca  ggagaagggg  gctctgagtg  atgatgat  tgtcagccct  600
tccatgcaat  tctacgaagg  tgccagggac  cgggatgaga  agaaggggcc  cctggagaat  660
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gcatcacctc  ctctcttgc  agtggaaact  tgtgcaaa  aatagatagt  tctgcctctt  1920
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agggcctgag  aggt ctacgc  tcttggagga  gggctaaggc  tttagcattg  tgaagcctg  2040
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tcacctgggg  cctagagtgg  aagtgggggt  gggttaacct  cacacaagca  cagatccag  2160
actttgccag  aggcaaacag  ggaattccgc  cgatactgac  gggctccagg  agt cgtccgc  2220
acactg

```

2227

<210> 331  
 <211> 254  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(254)  
 <223> 3' terminal sequence. macrophage stimulating  
 1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331  
 gcataaaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60  
 ggcatacaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120  
 gacacgcgtg aagacagctg gccagcggga ccttgccgat actcggttgg ggattataat 180  
 tccttcagg gaccagcag ttgtgggtaa agcaggcaag tgggccccg tagtcaccct 240  
 cacaggcccc caca 254

<210> 332  
 <211> 362  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(362)  
 <223> 5' terminal sequence. macrophage stimulating  
 1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332  
 gccatggncc tgggtctaca cgatggaccc aaggaccca t tgcactact gtgccctgcg 60  
 acgctgcgt gatgaccagc cgcacatcaat cctggacccc ccagaccagg tgcagtttga 120  
 gaagtgtggc aagagggtgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180  
 ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240  
 tcggggnggt ctctagtga ggaacagtn atactgactn cccggaagtg ctctcctccc 300  
 tnccatatnc ctctcacggg ctatgaggta tggttngggc ancctttttc cagaacccac 360  
 ag 362

<210> 333  
 <211> 2219  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(2219)  
 <223> macrophage stimulating 1 (hepatocyte growth  
 factor-like) (MST1) gene.

```

<400> 333
agccagaagg atgggggtggc tcccactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tcgccattga atgacttcca agtgcctcgg gccacagagc tacagcacct 120
gctacatgcg gtgggtgcccg ggcccttgga ggaggatgtg gcagatgctg aagagtgtgc 180
tggtgctgtg ggccctctaa tggactgcgc ggccctccac tacaacgtga gcagccatgt 240
ttgccaaact ctgccatgga ctcaacactc gccccacacg aggtcgcgcg tctctggggcg 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg 360
gtaccggggc accatgtcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggccctggaag agaacttctg 480
ccgtaacctc gatggcgac c cgggaggtcc ttggtgctac acaacagacc ctgctgtgcy 540
cttcacagag tgcggcatca aatcctgcgc ggaggccgcg tgtgtctggt gcaatggcga 600
ggaataccgc ggcggggtag accgcacgga gtcaggggcg gagtgccagc gctgggatat 660
tcagcacccg caccagcacc ccttcgagcc ggccaagtgc ctccaccaag gtctggacga 720
caactattgc cggaaacctg acggctccga gcggccatgg tgctacacta cggatccgca 780
gatcgagcga gagtctctgt acctcccccg ctgcgggtcc gaggcacagc cccgccaa 840
ggccacaact gtcagctgct tccgcgggaa ggtgagggc taccggggca cagccaatac 900
caccactgag ggcgtacctt gccagcgttg gaacgcga a atcccgcatc agcaccgatt 960
tacgccagaa aaatacgcgt cgaagacact tcgggagaac ttctgcggga accccgacgg 1020
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gatccggcgt tgtacagacg acgtgcggcc ccaggactgc taccacggcg caggggagca 1140
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gacgcgcgac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgcggg aaaccagatg gggatagcca tggccctcgt tgctacacga tggaccacaag 1320
gaccaccatt gactactgtg ccttcgcagc ctgcctgat gaccagccgc cat caatcct 1380
ggacccccga gccaggtgc agtttgagaa gtgtggcaag aggggtggatc ggctggatca 1440
gcggcgcttc aagctgcgcg tggttggggg ccactccggc aactcacctc ggacagtca 1500
cttgcggaat cggcagggcc agcatttctg cgggggggtct ctagtgaagg agcagtggt 1560
actgactgcc cggcagtgct tctctctc tg ccatatgcct ctacaggctc atgagctatg 1620
gttgggcacc ctgttccaga acccacagca tggagagcca agcctacagc gggctccagt 1680
agccaagatg gtgtgtggcg cctcagctc ccagcttgct ctgcctaagg tggagagatc 1740
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tccaggggac aagtgtgaga ttgcaggctg ggtgtgagac aaaggtacg gtaatgacac 1860
agtctaaat gtggcctttc tgaatgttat tccaaccag gagtgtaca tcaagcaccg 1920
aggacgtgtg tcggagagtg agatgtgcac tgagggactg ttggccctct tgggggctg 1980
tgagggtgac caggggggcc cactgcctg ctttaccac a actgctggg tctctgaagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgtcgc ccagctgtct tcacgcgtgt 2100
ctctgtgttt ttggactgga ttcaacaagg catgagactg ggttagggcc agcctgtatg 2160
ccatatgcct tggggaggac aaaactttct gtcagacata aagccatggt tctcttcta 2219

```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione  
s-transferase pi (GSTP1) gene.

<400> 334

```

gaaaggaagg caaactctgc ccccc gctca gactcccccc aaccctcact gtttcccggt 60
gccattgatg gggagggtca cgtactcagg ggaggccagg naggcntgna gtttgggcgg 120
ggcactgagg cgcgccacat atgctgagag cagggggaac gcattccaggc agccagggct 180
agggaccnca tggactcagc gcaagtccag caggttntag tcagcgaaag agnctgtgct 240
tcccacaatg aaggtctctgc ctccctggtt ctgggacacg agggcttcaa aaggcttcag 300

```

## 217/292

```

ttgcccgggc agtgccttca catagtcato ctgcccgcgc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggctg 420
nctcctttt t 431

```

```

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
        s-transferase pi (GSTP1) gene.

```

```

<400> 335
nattcggcac aggtcgccac catgcccgcgc tacaccgtgg tctatttccc agttcgaggg 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaaaga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct nacctgtgac cagt ccaata ccacctgtcg tcacctgggc 240
cgacccttgg ggctnctatg ggaaggacca gcaggangca gccctgggtg acatngtgaa 300
tgacg 305

```

```

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

```

```

<400> 336
ggagtttcgc cgcgcagtcg ttgccaccac tgccgcctca caccgtggtc tatttccag 60
ttcagggcgc ctgcgcggcc ctgcgcacgc tgctggcaga tcagg gccag agctggaagg 120
aggagtggtg gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatacgg 180
ggcagctccc caagttccag gacggagacc tcacctgtga ccagtccaat accatcctgc 240
gtcaacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctgggtg 300
acatggtgaa tgacggcggtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaaac cagggaggca agaccttcac tgtgggagac cagatctcct 480
tcgctgaact caacctgctg gacttgctgc tgatccatga ggtccctagcc cctgggtgcc 540
tggatcgctt cccctgctc tcagcatatg tggggcgct cagcgcccg cccaagctca 600
aggccttctt ggcctccctt gactacgtga acctcccat caatggcaac gggaaacagt 660
gagggtttgg ggaactctga ggggaggca gagtttgcct tctttctcc aggaccaata 720
aaatttctaa gagagct 737

```

```

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

```

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 337

```
gtggngctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaactctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggttttaa 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggcaggag 180
aaaccttcaa gaaacaagggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttgggt gaacaaaagc tcctcagtg gccagtgcaca 300
tcnnggttt ttcttagggg aggctgagga ctccaggggt tatctcaact tctcaggaa 360
gctttttgaa gg                                     372
```

&lt;210&gt; 338

&lt;211&gt; 508

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
cccccaact cccaataactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca tttcgggtgac ttccgcacga ggaaggctag agttaccag agcatcaggc 240
gcgcacaagt gcctgctttt aggagaccga agtcocgaga acctgcctgt gtcccagctt 300
ggaggcctgg gtccctgggaa ctgagccggg gccctcactg gccttcoctt caggggatgg 360
atcaacaggg gcagtggtgtt ctccogaatg totgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg ttgggtggg gcttggtcac ctgg gggggc 480
ttccaggtag ggcccttttt aagtggga                                     508
```

&lt;210&gt; 339

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(445)

<223> 3' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 339

219/292

```

tttttttant caaaagtgtg aaattcaagt aactttattt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctaggittaa ctgaccaga tctgactt tg gactttattc tttaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtact 240
ngnggtacaa ntttgggtga cagaaaaagac ttacaggtata tgctgggcat cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttctcat cctcgn tctt ggggnggcc aggtaggtnt tttaggtgtc cccntatccc 420
ganttttala ctctncaccg ggggg

```

&lt;210&gt; 340

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(437)

<223> 5' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 340

```

gtctccagct tgtaaacctg cagagatgga ctctgccac gtctcttttg tgcagctcac 60
cctgcggctct gaggcgcttcg acacctaccg ctgcgaccgc aacctggcca tgggggtgaa 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaaacca ggagaaagt 240
tcagactatg aaatgaaagt gatggattta gatgttgaac aacttngaatt tccagaacag 300
gagtacagct gtgtagtaaa gatgccttct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacggggagt gaaaattttt 420
ctgcaagtgg gagnaact

```

&lt;210&gt; 341

&lt;211&gt; 1231

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)  
gene.

&lt;400&gt; 341

```

aggtctcagc cggctcgtgc gacgttcgcc cgctcgctct gaggtcctg aagccgaac 60
tagctagact ttctctcttc ccgcctgcct gttagcgggt tgttgccact ccgccaccat 120
gttcgagggc cgctcgtgtcc agggctccat cctcaagaag gtgttgagg cactcaagg 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctctgccacc gtctcttttg tgcagctcac cctgcggctc gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaaatg 360
gccgcggcat gaagataatc ttactactaa ggccgaagat aacgcgggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttacagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgaa ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggatgaatt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

```

## 220/292

```

attgtcacag acaagtaatg tgcataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggtg cctgaact tc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtacc cttgtgtgag agtataaaa 840
tgccgataatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg ctcttaagat 960
gccagcatat actgaa gtct ttctgtgcac caaatittgta cctctaagta catatgtaga 1020
tattgttttc tgtaaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc tttagaaatc 1140
ttgtgtattt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg tttt 1200
gaatttaaat aaagtactt gaatttcaaa c

```

1231

&lt;210&gt; 342

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(383)

<223> 3' terminal sequence. adenovirus 5 el  
binding protein (BS69) gene.

&lt;400&gt; 342

```

ttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccogtgt 60
caacagagag agaaaagcca agtaaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga tttaacacca aaaatatct c cacaattact tgctctcata 180
ggggtggatc gaagtcctta aacttgaaaa acaatcaaa aaggttaagt gttctcggtt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacatgtgat ggaatggggg 360
gtctactggg gtactttt tac

```

383

&lt;210&gt; 343

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 5' terminal sequence. adenovirus 5 el  
binding protein (BS69) gene.

&lt;400&gt; 343

```

gttnaaattg cagggactgg ggtaaatctt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcactt ttgtcctaac atgagtgcct gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt cccctccctt cccacatc atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgcttat gtttgtaggt aatgggggtca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgttaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctcg gtattttgcy gggatgtctg gggttaggga ggccttacc ttaggggntg 480
ggg

```

483



<210> 344  
 <211> 2722  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(2722)  
 <223> adenovirus 5 ela binding protein (BS69)  
 gene.

<400> 344  
 ggagcataat gctaaagaag taaacaggtc atggcaactg taacaaaaag acgacaggcg 60  
 atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120  
 ttgccaaacat tgaccgttat acaaaatgtg aaacaactac attattcttg aacctatggt 180  
 gatttttaca tcaattacaca gatattgtcat ttctcattagt tgtatcattg ttataaactg 240  
 gtatatgtct cgagtcocag gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300  
 tgtgaaagat ggtctttattg tc gaaactct aacagtgggc tgcaaaaggtt caaaagctgg 360  
 tattgaacaa gaaggatattt ggttgccagg agatgagatt gactgggaaa cagaaaaatca 420  
 tgactggtat tgttttgaat gccatttgcc tggagagggt ttgatattgt acctgtgttt 480  
 tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540  
 ctggcagtc ccagtttgca ggagcattaa gaagaagaat acaaaacaa aggagatggg 600  
 cacataccct agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660  
 ggggaaggac aataaacacc cgatgtacag gaggctgggt cactcagctg tggacgttcc 720  
 caccattcaa gagaagaagt atgaagggaa ataccgaagt ta tgaagagt tcaaaagctga 780  
 tgcccaattg ctctccacca ataccgtgat ttcttatgga gcagacagtg agcaagctga 840  
 cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agcttttgcaa 900  
 gaattgcttt tactttgcac atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960  
 taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag caaaagctat 1020  
 gcgaagaag gacaaatcaa tcgacgttgc ctcttttggc caccacacc agcgggctgt 1080  
 gattcctctc gaaaacattc aagatatcac agtcaacatt catcggtctc acgtgaagcg 1140  
 cagtatgggt tggaaaaagg cctgtgatga cgtggagctg catcagcgtt tcttacgaga 1200  
 agggagattt tggaaatcta agaattgagga ccgaggtgag gaagaggcag aatccagtat 1260  
 ctctccacc agtaatgagc agctaaaggt cactcaagaa ccaagagcaa agaaaggagc 1320  
 acgtaatcaa agtgtggagc ccaaaaagga agaaccagag aagcagtaag 1380  
 ttctagccag gaaataccca cgatgcctca gcc atcgaa aaagtctccg tgtcaactca 1440  
 gacaaaaga ttaagtgcct cttoaccaag aatgctgcat cggagcacc agaccacaaa 1500  
 gcacggcgtg tgtcagagca tgtgccatga caaatacacc aagattcttca atgacttcaa 1560  
 agaccggatg aagtgcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620  
 gaagctgcgt tctgaaatgt agaagaataa gagacaagct gtataataag cgtgagccaa 1680  
 catgcaagggt gagatggaca gaaaatgtaa gcaagtaaa gaaaagtgt agaggagatt 1740  
 tgtgaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agtaccagaa 1800  
 gaagcagtg tgtacaaact gtgaggagga ggcattgtac cactgctg ct ggaacacatc 1860  
 ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gagcacaagc gcaactgcgc 1920  
 ccggaagaag tgaagctggc ccttcccgga ctgcaccoga tgattactct tttagcacac 1980  
 agcggttttt gtttccaaag agccaaaatt gtttagaatt tgcttcccat tttagcaccg 2040  
 ccgttaaaaa cttttctgta ag aaattttg cacagtattt taaacttttt gttaatgtct 2100  
 ctccgaagtt tttagggggg taaaagtaac atcagtgag ggtattattt taaataaatt 2160  
 ttaattgaga atttgttgca tttagcagaa atttttaggt atttttaggt tttagcagaa 2220  
 ttttaacctt taacaacacg atctttaaaa aacaggtgaa tacaagtgg ttttaacaaag 2 280  
 aaacatttag aatagatctg aatgtaagaa ctacagaact gttttcagaaa taaaacatac 2340  
 taccttgatg tgacattttt ttcttaacct gtgttgagctg gttttgtcca gcttaattta 2400  
 ctgtttcaag gcattatctg ttgtgtcaac cagtgggtat atgattgaa tttaggaaca 2460  
 ggggtgacac agcagggcta gctctgcaata tttttt cttta aatatttccc aatttgtgtt 2520  
 ttcatatttt cttttcaata tataactttt ataacaatt attagctttg atctttagt 2580  
 ttaaaatttg agggaactgg ggtaatcttt tactgagctg gatcttagag aaaaatgaata 2640  
 tttaaatttt aaagtttgac acatttccatc ttgtgctcaa cagtgtgct tgtacaacaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

&lt;210&gt; 345

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(363)

&lt;223&gt; 3' terminal sequence. matrix

metalloproteinase 11 (stromelysin 3) (MMP11) gene.

&lt;400&gt; 345

```
gcattgcagca tcttgtagtgg tagcgtcgat ctcagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgcgc ggtgctgggg tggaacgcgc agtagtccct 120
gcctcggaag aagtagatct tgttcttttc gggaccccag accaaggc ag catggaccgc 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgc cttttaccgc 240
tcgtacaccc agtacttgag caccttgggg agaaccaaat gtggggcccg cttaccaccg 300
attggccttt tcgccacagg gctggggcag tccctgcacg tngcgagaag ccaatttttg 360
gca                                     363
```

&lt;210&gt; 346

&lt;211&gt; 2260

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2260)

&lt;223&gt; matrix metalloproteinase 11 (stromelysin 3) (MMP11) gene.

&lt;400&gt; 346

```
aagcccagca gccccggggc ggatgggtcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg cccccgatgc tgctgctgct gctccagcgc ccgcgcgtgc tggcccgggc 120
ttctgcgcgc gactgtccac acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgcgc agtag cccgg cacctgcccc tgccacgcag gaagcccccc ggccctgccg 240
cagcctcagg cctcccgctc gtggcggtgc cgacctatct gatggctga gtgcccccaa 300
ccgacagaag aggttcgtgc ttcttgccgg gcgctgggag aagacggacc tcacctacag 360
gatccttcgg ttcccatgac agttgggtgc ggagcagggt cggcagacga tggcaga ggc 420
cctaaggata tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacataatg atcgacttcg ccaggtactg gcatggggac gacctgcgct ttgatgggcc 540
tgggggcata ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcaggtggc 660
agcccatgaa ttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtcgcgcttc tacacctttc gctacccact gactctcagc ccagatgact gcagggggct 780
tcaacacctc tatggccagc cctggcccac tgtcacctcc aggaccccag cctggggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgagccc tcctttgacg cgtctccac catccgaggc gactcttttt tcttcaaagc 960
gggctttgtg tggcgctcc gtggggggcca gctgcagccc ggctaccagc cattggcctc 1020
tcgcccactg cagggactgc ccagccctgt ggacgctgac ttcaggatg ccca gggcca 1080
catttggttc ttccaagggt ctagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcacc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccgag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccacco 1260
cagcaccccg cgtgtagaca gtcccgtgc c ccgcagggcc actgactgga gagggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc cccgtctcgt 1440
gggtcctgac ttcttttggt gtgccgagcc tgccaacact ttctctcgac catggcttgg 1500
atgccctcag ggggtcgtgac ccctgccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtggggac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtgggggtac aaccaccatg acaactgccg ggaggggccc gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg caggggaggct ttggcatgac tt aagaggaa gggcagtcctt 1740
gggaccgcct atgcagggtcc tggcaaacct ggctgccctg tctcatccct gtccttcagg 1800
gtagaccatc ggcaggactg ggggaactgg agtgctcttg ctgtatccct gttgtgaggt 1860
tccttccagg ggcctggcact gaagcaaggg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggcctgtaggg caggggccact tctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc agggcaaaaa 2040
gttcacagtc aaatggggag gggatttctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatctctgc ccaggccgga tcctcctgaa gcccttttgc cagcac tgct 2160
atctccaaa gccattgtaa atgtgtgtac agtgtgtata aacctttctt ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

&lt;210&gt; 347

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequenc e:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(273)

<223> 3' terminal sequence. hypothetical protein  
mgc13071 (MGCL13071) gene.

&lt;400&gt; 347

```

atgtttattg aacgtaacag tatatttcat gtatgttccc ataatttttt catgtactaa 60
tcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaagggtgg tgttacgaat 180
catcggggct gtggccagnt tgcttcacgg aggtgcaggg aggctggggc ctactaggg 240
canctggagg agcagggact gccctgccgg cag

```

&lt;210&gt; 348

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(330)

<223> 5' terminal sequence. hypothetical protein  
mgc13071 (MGCL13071) gene.

&lt;400&gt; 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaatattct ttgactcgtg ttctcaacca cgtagtgcnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```

224/292

```
cctgcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc ttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagccngg tgaagnacca 330
```

<210> 349  
<211> 1168  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:prime r

<220>  
<221> misc\_feature  
<222> (1)..(1168)  
<223> hypothetical protein mgc13071 (MGC13071)  
gene.

```
<400> 349
aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcagggtg tgagaggggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtcacat cggcaagttt ggccctggcct tagctgttgc aggagggcatg gtgacctctg 180
ccttatgtaa tctggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtagc 240
agaacattgtt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tcctttgactg ctgttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttacc 360
agaatgtcaa catcacactg tgcactctct tcgggcccac cactagccag ctctcccgca 420
tcctcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tctcaagtc actggtggtc cgctttgatg ctggagaact aatcacccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctcatcttgg 600
acgacgtgtc tttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcgccc atcatctctg ctgaggggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggagc gccagagcga 7 80
gctgtgtcaa ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgacctg ccggcagggc agtccgtgct cctccagctg ccctagtagg gcccccagct 900
acctgcacct ccgtgagcca actggggccac agccccgatg attcgtaaca ccacctttcg 960
ccctcaccctc agaatacact gaaatttcat gattggctta aagtgaagga agtaaaagga 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaa aaaaaaaaaa aaaaaaaa 1168
```

<210> 350  
<211> 315  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(315)  
<223> 5' terminal sequence. interleukin enhancer  
binding factor 2, 45kd (ILF2) gene.

```
<400> 350
ctggccttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
ccaactcttc gaaaacttga tcagaactc catttggata tcaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctgggtc gaggaaaatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggaacttga gattcgttt ccnggctttg agc cctcaca 240
```

225/292

ccenggatnc ttgaactact aggcattat gctgtgatga acaaccac caganagcct 300  
 ttgcnctaa acgtt 315

<210> 351  
 <211> 1552  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1552)  
 <223> interleukin enhancer binding factor 2, 45kd  
 (ILF2) gene.

<400> 351  
 cggttggtgc ggcctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60  
 ggtcgtgggt ggcgcttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120  
 ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180  
 cctgatgaaa ctctcttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240  
 tctgctgaac aggcattctat cctttctctg gtgacaaaaa taaacaatgt gattgataat 300  
 ctgattgtgg ctccagggac a ttggaagt caaattgaag aagttcgaca ggtgggatcc 360  
 tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgt gatactcaag 420  
 attctgccaa cgtttgaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480  
 gcacaggatc cttctgaagt tttaaccatg ctgaccaacg aaactggcct tgaatatcagt 540  
 tcttctgatg ctacagtgaa gattctcatt acaacagtg cacccaatct tcgaaaactg 600  
 gatccagaac tccatttga tatcaaaagta ttgcagagtg ccttagcagc catccgacat 660  
 gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagtctcat cagctctcat 720  
 aaggacttga ggattcgttt tcttggtctt gagccctca c acctggat acctgacctg 780  
 ctaggccatt atgctgtgat gaacaacccc accagacagc ctttggccct aaactgttga 840  
 tacaggcgct gcttcgagat tctggctgca ggactgttcc tgccaggttc agtgggtatc 900  
 actgacccct gtgagagtgg caacttttaga gtacacacag tcatgacctt agaacagcag 960  
 gacatggtct gctatacagc tcagactctc tccgaatcc tctcaactgg tggctttagg 1020  
 aagatccttg gccaggaggg tgatgccagc tatcttgctt ctgaaatate tacctgggat 1080  
 ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaaagg 1140  
 gaggaagaag aggagaatac agaaagaacc acctcaagg gaggaagaag aaagcatgg a 1200  
 aactcaggag tgacattccc ttcaactcct ttctaccca agggaagac tggagcctaa 1260  
 gctgcctgct actgcgttta catggtgaca gacattccgt ggataggaag atagcaggag 1320  
 aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagctcccca 1380  
 ttttgcacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440  
 taattcccaa ctccgtaaaa aactaatact ttgctgttga aatgttgta 1500  
 aatgttaagt gtcctgaaat ttttttttct aagaaaaact attaaagtac tt 1552

<210> 352  
 <211> 396  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(396)  
 <223> 3' terminal sequence. hypothetical protein  
 flj11307 (FLJ11307) gene.

226/292

<400> 352  
 ctccattaca gggtttttgc cacttgcgtg gaggataggg cctcgagttc ttacctctaa 60  
 ggtactggag gtttcagttg tagaatttcc agtattattg ctgagtttg aagacactgt 120  
 ttcatittta ctttcattat ctgatttttc atcggaaetc atacattcaa tatctgcac 180  
 aaagcctgtt ggatatacca ttgcttgcaa taccttcacc gctacgtgaa agttttgctg 240  
 ttttcttgga tggctctgag gcttcataat ttgtgccatc cacatctaca gacattg tga 300  
 agactggggg catgaacggg gccacgactg aagataagaa gctactactga agcacagggc 360  
 tgatctgaat taagcntcat tagtggcatt ccataa 396

<210> 353  
 <211> 1858  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<220>  
 <221> misc\_feature  
 <222> (1)-(1858)  
 <223> hypothetical protein flj11307 (FLJ11307)  
 gene.

<400> 353  
 tcgatgaag atcctccgga cttattggac aggcagaat gccgaacgc ctggcgctct 60  
 ctctgcacat ccaaatgggt tcaggcaagg gcaaatggat taaatcatg tgtaat tgct 120  
 ctccgcatc tgctgtattt gtgcaacaga gtccccacat gggcaccatt gaaaggtagg 180  
 ccactagaac ttatagtga aaagtctata ggtacttgta atagaccttt gggcgtgggg 240  
 gaggccttga gacgagtaat ggagtgtttg gcactctgaa tactacttcc tgggggtctc 300  
 ggtcttcagt atccttgtga gcgagaccga acag atgctc tgagctatat gaccatccag 360  
 caaaaagaag atattacca cagtgcacag catgcactca gactatcagc ctttggccag 420  
 atttcaaa tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480  
 ttgtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540  
 ggattagggg atgataaaga cccaacaag aagatgaac gaaacttaag gaaaattctg 600  
 gatagtaaa caatagacct tatgaatgca ctaatgaggg taaatcagat caggcctggg 660  
 ctccagtata agctctctac tcagtctggc cccgttcatg ccccgactct cacaatgtct 720  
 gtatgtgtg atggcacac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780  
 cactagcgg tgaaggtatt gcaggcaatg ggatatccaa caggctttga tgcagattt 840  
 gaatgtatga gttccgatga aaatccagat aatgaaagta aaatgaaac agtcttctca 900  
 aactcaagca ataactcgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960  
 actcagggcc ctatctctac agcaagtggc aa aaacctgt taatggagct caatgaaaa 1020  
 agaagaggtc tcaagtatga actcatctca gagactgggt gaagccatga caagcgcttt 1080  
 gtaattggag tagaagtaga tggacagaaa tccagaggcg caggctccaa taagaaagt 1140  
 gcaagggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200  
 aatataaaga aaaagaagat tatcctcag gcaagggcg ttgtgaatac agctgtgtct 1260  
 gcagcagtc aaagctgttc gggcagagga agaggaactc taacaagggg agcttttgtt 1320  
 ggggcgacag ctgctccttg ctacatagct ccaggctatg gaacaccata tggttacagc 1380  
 acagctgcc ctgcctatgg ttaccacaag agaattgttc tttac cgt tatgaaattt 1440  
 caacatata ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500  
 tgaacaacaa tacagttaca cagagaatgt tagagaaaaa cgtgttttat cctgtttct 1560  
 ttgaacacat acttgatcaa aattatttgt aaagaacatc tttctactt tttgatttta 1620  
 acaaatgcga atttagttct ctaaaacttg aaaaaaaaaa aagaacacag tctgtgaaa 1680  
 accgtacctc atttctggaa aataacttat accagccctt ctgttctagg gaataaaaag 1740  
 tctagcagtt caaagtttta gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800  
 gaaggatgta tagagtctca aacactgatc acaaataaac tgctttgttg taacacag 1858

<210> 354  
 <211> 242  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(242)

<223> 5' terminal sequence. v -myb avian  
myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaaccccg cttacaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                     242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene  
homolog (MYB) gene.

<400> 355

```
ggcggcagcg cctcgccgac gccggggagg gacgcaggca ggcggcgggc agcggggaggc 60
ggcaccccg tgctccccgc ggtctctcgg ggagccccgc cggccgcgcg gccatggccc 120
gaagaccgag gcaca gcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg ctccccaagt ctggaaaagcgc tcaacttgggg aaaaacaagg 240
ggaccgggga agaggatgaa aaactgaaga agctgggtgga acagaatgga acagatgact 300
ggaaagtatt tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat gcc 360
agaaagtact aaacctgag ctcatcaagg gtccctggac caaagaagaa gatcagagag 420
tgatagagct gtacagaaaa tacggtccga aacgttggctc tgttattgcc aagcacttaa 480
aggggagaat tggaaaaaaa ttaggggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt atta ccaggccacac aagagactgg 600
ggacagatg ggcagaaatc gcaaaagtac tgctgggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttccagaa gaacagtcac ttgatgggtt 780
ttgctcagcg tccgcctaca gctcaactcc ctgccactgg ccagcccaact gttacaacag 840
actattccta ttaccacatt tctgaagcac aaatgtctc cagtcatggt ccataccctg 900
tagcgttaca tgtaaatatt gtcaatgtcc ctacgccagc tgccgcagcc attcagagag 960
actataatga tgaagacctc gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgatgta aaggacagc aggtgctacc aacacagaaac cacacatgca 1080
gctacccagc gtggcacagc accaccattg ccgaccacac cagacctcat ccagacagtg 1140
cacctgttcc ctgtttggga gaacaccact ccactccatc tctgccagcg gatcctggct 1200
ccctacctga agaaaagcgc tcggccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tggataatgt taagaacctc ttagaatttg cagaacacct ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaaat gcctcttcta acttccacc 1380
ccctcatttg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaacc cagctatcaa aaggtcaatc ttagaagact 1500
ctccaagaac tctacacca ttcaaacatg cacttgcagc tcaagaaatt aaatacggct 1560
ccctgaagat gctacctcag acacctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc  tgaatgaatc  ggatttggtg  ctgagtttca  aga  aaatgga  ccacccttac  1630
tgaagaaaaa  caaacaagag  gtggaatctc  caactgataa  atcaggaaac  ttcttctgct  1740
cacaccactg  ggaaggggac  agtctgaata  cccaactgtt  caccgagacc  tcgcctgtgc  1800
gagatgcacc  gaatatcttt  acaagctccg  ttttaatggc  accgacatca  gaaqatgaag  1860
acaatgttct  caaagcat  tt  acagtaccta  aaaacaggtc  cctggcgagc  ccccttgagc  1920
cttgtagacg  tacctggaaa  cctgcatcct  gtggaagat  ggaggagcag  atgacatctt  1980
ccagtcaagc  tcgtaaaatc  gtgaatgcac  tctcagcccg  gacgctggtc  atgtgagaca  2040
tttcagaaaa  agcattatgg  ttttcagaac  agttcaagtt  gacttgggat  atatcat  tcc  2100
tcaacatgaa  acttttcatt  aatggggaga  gaacctattt  ttgttgtggt  acaacagttg  2160
agagcacgac  caagtgcatt  tagttgaatg  aagtcttctt  ggatttcacc  caactaaaag  2220
gatttttaaa  aataaaaatac  agtcttacct  aaattattag  gtaatgaatt  gtgaccagtt  2280
gttaatatct  taatgcagat  ttttttaaaa  a  aaaacataa  aatgattttat  ctgggtatttt  2340
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aaaggctactc  cagtatcttca  cttttctcga  tcactaaaca  tatgcatata  tttttaaaaa  2460
tcagtataag  cattactcta  agttagact  taataccatg  tgacatttaa  tccagattgt  2520
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agttttctgt  tagcttgctt  taaaaattat  tactgtaaga  aatagtttta  taaaaaatta  2640
tatttttatt  cagtaattta  attttgtaaa  tgccaaatga  aaaacgtttt  ttgctgctat  2700
ggcttagccc  tcttagacatg  ctgctagtat  cagaggggca  gtaga  gcttg  gacagaaga  2760
aaagaaactt  ggtgttaggt  aattgactat  gcaactagtat  ttcagacttt  ttaattttat  2820
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attttttatt  gtggtttttt  tgtttattgt  ggtttataca  agcatgcgtt  gcacttcttt  2940
tttgggagat  gtgtgttgtt  catgttctat  gttttgtttt  gtgtgtagcc  tgactgtttt  3000
ataaattggg  agttctcgat  ttgatccgca  tcccctgtgg  ttctcaagtg  tatggctcca  3060
gaaactgttg  atggatcctg  tgtttgcaac  tggggagaca  gaaactgttg  ttgatagcca  3120
gtcactgcct  taagaacatt  tgaatgcaaga  tggccagcac  tgaacttttg  agatatgac  g  3180
gtgtacttac  tgccttgtag  caaaaataag  atgtgccctt  atttt  3225

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&lt;210&gt; 356

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9  
(a cellular retroviral nucleic acid binding  
protein) (ZNF9) gene.

&lt;400&gt; 356

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gtagttaaat  gcagaaagtc  ggtttttttc  cacccttttc  ctctttttac  acggcaagta  60
aagctcactg  gctctgggag  tgctctatc  tgccaacctt  tggccagtga  agaggattca  1 20
gagaaaaata  tacaaccatc  aatcagaaaa  aggaggggag  acaaaggaaa  ataattagcg  180
tgtagctcaa  ttgtgcattc  ccgtgcaagg  tgccctgact  cgccacagcg  gtaacagttg  240
acttcacttg  tcttctgtca  gttagtggt  acatgaccag  ttccaccaca  cctatagcac  300
ttcaacttgg  tgcagttctt  ttgtaatgt  tcccgaaatc  tcccacaaga  atanactttc  360
tgctcanct  369

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&lt;210&gt; 357

&lt;211&gt; 1500

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer



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<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
      nucleic acid binding protein) (ZNF9) gene.

<400> 357
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ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccactggggc cgggaatgtc ctactggttg aggcgcgtgt 180
cgtggaatga gaagccgtgg cagaggtggt tttaacctgg atagaggttt ccagtttgtt 240
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctggctcatc tgccaaggat 300
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgctgtaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttgttg agaaltcgga 480
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tggtcatgta 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcaggggcac 600
cttgcacggg aatgcacaat tgaggctaca gcctaattat ttctctttgt cgccctctct 660
ttttctgatt gatggttgta ttttttctc tgaatcctct tcactggcca aaggttggca 720
gatagaggca actcccaggc cagtgcgctt tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaaacc gactttctgc atttaactac aaaaaaagtt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaacc ctttccgtg ccactggtga ataggagattg 900
atgaatggga agagtttgagt cagaccagta agcccgctct gggttcctat aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaaataa catcaagtaa 1080
catctgtatc aggcctatac tagaacatac agttgagtgg gagtaaacaa aaagataaac 1140
atcgctgtta atggctgttc gagagaaatc ggaataaaag cctaacacag acaacttcca 1200
tcacagtggt gatggttggc acatagatgg tgatggcaaa ggtttagaac acattatttt 1260
caaagactaa atctaaaaac cagagtaaac atcaatgctc agagttagca taatttggag 1320
ctattcagga attgcagaga atgcattttt cacagaaatc aagatggtat tttgtatata 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaaag tcaga tggaa 1440
agagcaactg aagtcctaga aatatgaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
      element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaaactg tagtaaatgt 60
tcagatatatt aaatgagcac caaacactac aaagtgcac caacatggtt ctattaaaaa 120
ctcnctttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaataataa aaatctgcaa atgccatata ttcatatcta ggctattctt cncatatagg 240
catgtcatta gatagaacct ctttctatct ttcccgagg natttttttg nggtttacnt 300
ttatgnaact gctggatgca ttatttttga tcatcctttc ctaaaagntt ttaaaagact 360
gcaaataatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
gtggc 425

<210> 359

```

<211> 332  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(232)  
 <223> 5' terminal sequence. camp responsive  
 element modulator (CREM) gene.

<400> 359  
 ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60  
 agcttttctt gtagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120  
 gaaacagctc atgaactgt aatgcatgaa cagaactcag gaggttgtctg gccagcttag 180  
 tgctgccact ggtgacatgc caacttacca gatcagagct cctantgnng ct 232

<210> 360  
 <211> 1431  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:prime r

<220>  
 <221> misc\_feature  
 <222> (1)..(1431)  
 <223> camp responsive element modulator (CREM)  
 gene.

<400> 360  
 atgaccattg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60  
 agcaagtctg ctcatgtgca gactcagact gggcaaatat caatccctgc tttagctcag 120  
 tgcagtgcgc tgagatcagg caccagaaga gggtccccag ctgtaactct agtgcagtta 180  
 ccttcggggc aaactataca tgtccaggga glaattcaga caccacagcc atgggttatt 240  
 cagtcatacg aaatcacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300  
 gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360  
 tataggaaaa tactgaatga actgtctctct gatgtgcctg gtgttcccaa gattgaagaa 420  
 gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480  
 atatatcaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540  
 tetaaccagg gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600  
 gctcctccac cagggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660  
 cagttctctt tcccaggcag ccagggttgtt gttcaagctg ccactggtga catgccaaact 720  
 taccagatcc gagctcctac tgcgtgcttt ccacagggag ttgtgatggc tgcacgcgcc 780  
 ggaagtttgc acagtcccca gcagctggca gaagaagcaa cagcgaacag agagctgagg 840  
 ctaatgaaaa acagagaagc tgcccgggag tgtgcaggga agaagaaga atatgtcaaa 900  
 tgtcttgaaa atcgtgtggc tgctcttgaa aaccaaaca agactctcat tgggaacctc 960  
 aaggccctca aagatcttta ttgccataaa gttagagtaac tgtctttgac ttggaccttg 1020  
 tttactctaa tcaaggcagc agatgcagca gtctacttta ttgccatgtg gacttgttgg 1080  
 aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140  
 tgttgttcca ggaatgtggaa tgcagcgtga tcacacttac cgagcttact ttgactctgt 1200  
 tgtcaatagc atgcaaaaaa tgcctttgct gccctttgct tctgcttttt tcaggggaag 1260  
 ctgccaagaa atgtgcagct cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320  
 cagtgctgga agtccagaac aagaagctta tagaggaact tgaacccttg aaagacattt 1380  
 gttctcccaa aactgattac tagaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361  
 <211> 457  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(457)  
 <223> 3' terminal sequence. cathepsin b (CTSB)  
 gene.

<400> 361  
 caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca ggggaagct 60  
 gtaatttttc aaaaacagta aaagctggtt tctcctaaac tattttcctt gtggtagtag 120  
 agatcagtggt gtcagaaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180  
 gaggcaatct gtaaaaactag cacaggtctc ccgctgttcc actggctcac ccacatg att 240  
 agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300  
 gagggtgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360  
 agggctccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420  
 gaggtagctgg gggaactgat gggggaactt tcatac cg 457

<210> 362  
 <211> 401  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(401)  
 <223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362  
 atcatgcatt gcaacattta ttgatggagt tttoccaatt taatatttct catcatttcc 60  
 tcacatgatt agtaactgcta gcggacctac taaaatttta acactgactt attattagag 120  
 atggccttgc tttttcttac accattccaa aggagaacat tagatgtctg tattaatttc 180  
 aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgct g gcnccttaag 240  
 tgaataagggt ggtggtgact gttctgcaga gagtttctca taagcaggtg gagcattggg 300  
 aaccacaggt tcacagtttt ttctctgaag agacactttg ctgtcccgat gatcaaaccc 360  
 ttcttgtggg catcttctctg ttaaggcaca ttgaggccaa c 401

<210> 363  
 <211> 370  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(370)  
 <223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

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<400> 363
attaaggaag gtgtcctgtg ccttgaccct acaagatgcc aagagaagat gtcacttca 6 0
tctatggtta ccccaagaag ggacacggcc actcttacac cacggctgaa gaggccctg 120
ggatcggcat cctgacagtg atcctgggag tcttactgct catcgctgt tggtattgta 180
gaagacgaaa tggatcacaga gccttgatgg ataaaaagct tcatgtttgg actcaatgtg 240
cttaacaaga agatgccac aagaagggt tgatcatcgg gacagcaaa tgctctctca 300
agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc
370

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&lt;210&gt; 364

&lt;211&gt; 1524

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1)-(1524)

&lt;223&gt; melan-a (MLANA) gene.

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<400> 364
agcagacaga ggactctcat taaggaaggt gtctctgtgc ctgaccctac aagatgccc 60
gagaagatgc tcacttcac tatggttacc ccaagaagg gcaacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgt cctggggagtc ttactgtctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300
acagcaaatg gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcaccttaa gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tcttttggaa tgggttagga aaaaatgcaag ccactctctaa taataagta 540
gtgttaaaat tttagttagt ccgct agcag tactaatcat gtgagggaaat gatgagaaat 600
attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgactactatc tgtgccagag 660
gtaatttagg taaatccatg gtgttatttt ctgagagaca gaattcaagt ggggtattctg 720
gggccaatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttctga 780
accttgaccg acatgaactg tacacagaat tgttccagta ctatggagtg ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttactactaca ataataatt gtaaagatcc 960
tatagctctt tttttttgag atggaggttc gcttttgttg ccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctcgcgct ccagggttca agcaattctc ctgcctttagc 1080
ctcctgagta gctgggatta caggcggtgcg ccaactatgcc tgactaattt tgtagtttta 1140
gtagagacgg ggtttctcca tgttggtcag gctgggtcca aactcctgac ctacagtgat 1200
ctgcgcgcct cagcctccca aagtgtctga attacaggcg tgagccacca cgctcggtcg 1260
gatcctatat cttaggttaag acatataacg cagtctaatt caatttcaact tcaaggctca 1320
atgctattct aactaatgac aagttatttc tactaaacca gaaatttgta gaaggattta 1380
aataagtaaa agctactatg tactgcctta ctgctgatgc ctgtgttact ccttaaatg t 1440
acctatggca attagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg
1524

```

&lt;210&gt; 365

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:p rimer

&lt;220&gt;

233/292

<221> misc\_feature  
 <222> (1)..(556)  
 <223> 3' terminal sequence. apr -1 protein (APR-1)  
 gene.

<400> 365  
 actattcgtt aggcctttat tttctctat gttctgcagt aactaaggaa aatcatggta 60  
 aatgtcaatc ttcacacaa acgacagaca aagggtttca gaaacgtcag atatgaag aa 120  
 atctccatc ctctcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180  
 ctataagtg tgtacaagat catagattat gatggaacga ctctatttta gaacgttagc 240  
 aaaaactgta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300  
 ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa tttccatta 360  
 tcaaaaagca aacactctat ttgcgagttg aacaatgato actgatocaa aatatcnaat 420  
 acagtggtcc cgcccccoaa tcgacatcat ttccactta gggaccctgg catccactcc 480  
 ctgggggtac cegtgaectc nccctttacac cccccagggg ctggcctcag atctacctaa 540  
 gggnggggat aacc cc 556

<210> 366  
 <211> 464  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(464)  
 <223> 5' terminal sequence. apr -1 protein (APR-1)  
 gene.

<400> 366  
 aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60  
 cgtcagcaca gcatctttgg agatccgaag aagatcgta cagaagagtt tgtgcgcaga 120  
 gggtagctga tttataaacc ggtgccccgt agcagtcagg tggagtatga gttctctgg 180  
 gggccccgag cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240  
 cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300  
 gaggttgagg ctatctcctaa ttcagggtgt aggggttatt cgcgccctta agtagatctg 360  
 gaggcagacc ctgtgggggtt gtaaaagaga gtnacaggta cccccaaagg agtagatg nc 420  
 aaggggcccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367  
 <211> 1476  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1476)  
 <223> apr-1 protein (APR-1) gene.

<400> 367  
 ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60  
 tgcagctgcg gcaagtgctg gcggcggctg ctgcgcgaag tcagctggcg tgggaaactac 120  
 cctttgtagc tgagaacggc ttgtttattg ctacaaagac tctattgaca ttggtagctt 180  
 cagcggcagc agcttct tac ggtataaagc tgttgcttc tgaagaggct acaagcatcc 240

234/292

```

ttccctagga ctgctgtaag ctttgagcct ctgacaggag acatgcctcg gggacgaaag 300
agtcggcgcc gcctgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gccctctgtg tagcgagcac ccccgaaga c 420
gacctgagcg gcccgagga agaccogagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcactgcccc agcacaaaag ccttcagtgcc ccgggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcctcatggg caacagcgcc 600
aaggaagctc tggctctggaa agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttt gagatccgaa gaagatcgct acagaagagt ttgtgcgca agggtagctg 720
atttataaac cggtgccccg tagcagtcgg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccca 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtccctaagt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttccgtttgt tgagaataac aatatgttta aaaataaat tgaacaaatt ttttctttg 1200
ttctctgta ttgacattta gtataacagt tttgtcaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaaa aatgttgaa gaggatggag gatttcttca tatctgaagt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttctcta gttacttgac 1440
gtcttgtatc tctttttatt ttccgattgc ttatca 1476

```

&lt;210&gt; 368

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(436)

<223> 3' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 368

```

cgtttttttg ctttaaatac caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaataa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggt tcccaa gagt agccatggtt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggttaa tatttcagat tcagctagaa gacttttcca atgtttaaga tgtattttta 360
acccttaatg gttttagcct ccccaactta gctacttac ttttcnaagg gttttgtatt 420
tttcaacaaa ttgtgc 436

```

&lt;210&gt; 369

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

<223> 5' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

```

<400> 369
ggttgtctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aaggtggctg gagagcgata 120
cgtctacaaa ttgtctctgt acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gagggaggaca cctgcccgt 240
gaccacattt gaagacagcc ccgcttacct cctggacatg gacgctgca gcagcctccc 300
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnggc agtggngttt gtt ttgtgtt tttt 414

```

```

<210> 370
<211> 249
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(249)
<223> 5' terminal sequence. cd69 antigen (p60,
        early t-cell activation antigen) (CD69) gene.

```

```

<400> 370
ataataaggga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtgatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgcttt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
ccnagacgc 249

```

```

<210> 371
<211> 1702
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(1702)
<223> cd69 antigen (p60, early t-cell activation
        antigen) (CD69) gene.

```

```

<400> 371
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcattccg agagtggaca agaaaatgat gccaccagtc cccattttct aacagctcat 180
gaagggtcct tccaaatttc tgtcctgtgt gctgtaatag atgtgggtct catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggtaccag 360
aggaatgtct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
ttgaaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgcag gtatagagga acactggggt ggactgaaa aggaacctgg tcacctatgg 540
aagtgtgtcaa atggcaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaacac cttacaaata ataggaagaa atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagctcttc cataga gact 780

```

236/292

```

ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagAAC tatggaaaaa 840
aaggagaGaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacagggtga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaA ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtA ctagatactg aatgtaaaCa aaggaattat ggctggtaac ataggttttt 1140
agtctaattg aatcccttaa actcagggag catttataaa tggacaAatg cttatgaaac 1200
taagattttg aatattttct tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggagatg cgtgtaittA tttttttact tccctagctg tagacaggtc 1320
cttttcgatg gtacatatatt ctttgccctt ataactcttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaaC 1500
aatactagtc ttataatagg ttgtgactt tctctaaatca attctattac gtgcaatagt 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaa aaaaaaaaaa aa
1702

```

```

<210> 372
<211> 585
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(585)
<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

```

```

<400> 372
gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taactcttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatgggtga tcatattgtc aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcttgccctg tggtagctaa 360
aacTgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcnng tgaaggagga cattcctggc cctggaaatt tcnngataaa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgcnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctcnc cggggtaccg gcc ng 585

```

```

<210> 373
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

```

```

<400> 373
gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

```



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```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagtcccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaa acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcatacgca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaagaa aagccagaaa gctg cattgt g 451

```

&lt;210&gt; 374

&lt;211&gt; 425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing function and indian blood group system) (CD44) gene.

&lt;400&gt; 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctotga 60
caaaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c ttgtgtgc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaagcaat gccacgggat taggctatgg aagggaacaaa tggaccatt 300
caaatctct cccagggacc aggccctatt aacctggga aatgtcctta gctggtgggg 360
gaaaggttgg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
acccg 451

```

&lt;210&gt; 375

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing function and indian blood group system) (CD44) gene.

&lt;400&gt; 375

```

ggcgttccag ttccacttg gaggccttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctcggg aggaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggg attgctttcc actgaggttg ggggttgggg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa ttttcagat gcttctggga gacacccaaa 300
gggggaagct atttatctgt agtaaatcat ttatctgtgt ttttgaataa taaacctgt 360
gatcagtcct ttgatcagta taaatttttt aaagttaact ttgtcagagg caccaaaggg 420
tttaactga ttcataaata aatatcngga ctctctcgat ctccaaaaa aaaaaaaa 478

```

<210> 376  
 <211> 1794  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1794)  
 <223> cd44 antigen (homing function and indian blood group system) (CD44) gene.

<400> 376  
 ccgcgcacct cgttcgctc cggacacct ggacaagttt tgggtggcacg ca gcttgggg 60  
 actctgcctc gtgcgcctga gcttggcgca gatcgatttg aatataacct gccgctttgc 120  
 aggtgtattc cagctggaga aaaatggtcg ctacagcadc tctcggacgg aggcgcctga 180  
 cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240  
 catcgattt gagacctga ggtatgggtt c atagaaggg catgtgtgtga ttccccggat 300  
 ccaccccaac tccatctgtg cagcaaaaca cacaggggtg tacatcctca catacaacac 360  
 ctcccgatg gacacatatt gcttcaatgc ttccagctcca cctgaagaag attgtacatc 420  
 agtcacagac ctgcccgaat cctttgatgg accaattacc ataactattg ttaacogtga 480  
 tggcacccgc tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540  
 caacccctact gatgatgacg tgagcagcgg ctctccagat gaaaggagca gcacttcagg 600  
 aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660  
 gatcacggac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720  
 tgggggggtc cataccactc atggatctga atcagatgga cactcacatg ggagtcacga 780  
 aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840  
 catcttgga ctcctcttgg ccttggcttt gattcttga gtttgcattg cagtcaacag 900  
 tcgaagaagg tggggcgaga agaaaaagct agtgatcaac agtgccaatg gagctgtgga 960  
 ggacagaagg ccaagtggac tcaacggaga ggcagcaag tctcaggaaa tgggtgcattt 1020  
 ggtgaacaag gagtctgcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080  
 cctgcagaat gtggacatga agattgggtt gtaacaccta caccattatc ttggaaagaa 1140  
 acaacggtt gaacataaac cattacaggg agctgggaca cttaacagat gcaattgtgt 1200  
 actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260  
 tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320  
 cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcctcctcg 1380  
 ggtgtgctat gtaggtcttc taacaaaaac tacacatag tatctcctgat cgccaacctt 1440  
 tccccacca gctaaggaca ttccccaggg ttaattagggc ctggtccctg ggaggaaatt 1500  
 tgaatgggtc cattttggcc ttccatagcc taatccctg gcatgtcttt ccactgaggt 1560  
 tggggtgtac tagttacac a tcttcaacag accccctcta gaaatttttc agatgtctct 1620  
 gggagacacc aaagggtgaa gctattttat tgtagtaaac tatttatctg tgtttttgaa 1680  
 atattaaccc ctggtacagt cctttgatca gtataattt ttaaaagttac tttgtcagag 1740  
 gcacaaaagg gtttaactg attcataata aatatctgta cttctctgat cttc 1794

<210> 377  
 <211> 452  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(452)  
 <223> 3' terminal sequence. cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase) (CDKN3) gene.

```

<400> 377
ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggttt catttcaata caaatttatg tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattctt ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgcccg gactctctta ggtctcgag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagttaga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgatt aagggttttc cggtaatTTT t aaggcaggt tgtaagcncT tccattattt 420
cacagcagct ggccatgtcn ggagtcctcc ca 452

```

```

<210> 378
<211> 472
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(472)
<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 3 (cdk2 -associated dual
specificity phosphatase) (CDKN3) gene.

```

```

<400> 378
ggcagcgagcg gcaactggtc tgcagctggg gcggccanga ctgaagccca ngnttcaata 60
caaacaaagt agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggcctatctt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggtt gtaaaatttaa agatgittaga agaagtgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatTTTgt tttctgcacc agaggggaac tgtcaaaata 300
tagagtcoca aaccttctgg atctctacca gcaatgtgga attatcaccc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaataaatg gaagagctta 420
caactgcct taaaaattac cgaaaacct taatacactg ctatggagga ct 472

```

```

<210> 379
<211> 639
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(639)
<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

```

```

<400> 379
atggagcgc cagttcaat acaaaacagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgtctt 120
cagtttctcg gtttatgtgc tcttccaggt tgtaaatTTa aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatTTgt tttctgcacc 240
agaggggaac tgtcaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcaccc atcatcatcc aatcgcagat ggagggactc ctgacatagc cagctgctgt 360
gaataatTg aagagctTac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

```

## 240/292

```

tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tctactata cctgtctgac 480
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
tcatcaagag attcacaatc aagatctgta tcaagataa 639

```

```

<210> 380
<211> 487
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(487)
<223> 5' terminal sequence. max -interacting
protein 1 (MXI1) gene.

```

```

<400> 380
aagtggcgac tggaaacgct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
attggatcaa ctatttcttc agatcgttct gattcagagc gagaggagat tgaagtggat 120
gtgaaagaca cagagtcttc ccattggagaa gtggacaata taagtaccac cagcatcagt 180
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240
gtgtcaaac ttcattcact tcatagaacc cagcatgaca taacagtgca gggaaaaat 300
tcactgggcc attcatacaa acaatctctt aaattgggt catgatgcag tctctcttt 360
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
catttta 487

```

```

<210> 381
<211> 2416
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(2416)
<223> max-interacting protein 1 (MXI1) gene.

```

```

<400> 381
agattatgat cgcttgaggc cctctccta cccagatacc gatgttatac tgaigtgttt 60
ttcctttttt tttttttttt ttttaagtaat taagggtagt taaattattt aaagtataca 120
aagtccaaac agccagggggt aaggtctcca agaggccttc ccagggttagg ggaagtgcga 180
gagggcccg tgccaccocg cggtgcccat ggagcgggtg aagatgatca acgtgcagcg 240
tctgttgag gctgccaggt ttttgagcg ccgggagcga gagtgtgaac atggctacgc 300
ctcttcattc cgtccatgc cgagccccc actgcagcat tcaaaagccc caggagggtt 360
gagccgggca cagaacaca gcagcgggac gagcaacacc a gcactgcc acaagatctac 420
acacaatgag ctgaaaaaga atcgacgagc tcatctgcgc ctttgittag aacgcttaaa 480
agttctgatt ccactggagc cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
gaatttggaa cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctctca 660
ggagatggaa cgaatacgaa tggacagcat tggatcaact attcttcag atcgttctga 720
ttcagagcga gaggagattg aagtggatgt tgaagcaca gattctccc atggagaagt 780
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagc tgccagat 840
tgggagtgcaggagggttact ccagtgcag tgtcaaaact tcattcact catagaaccc 900

```

```

agcatgacat aacagtgcag ggcaaaatat tcactggggc aattcaatac aaacaatctc 960
ttaaattggg ttcatgatgc agtctctctt ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgaacaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggcatttgg 1200
agatgccatc ctctttctct tttctcgttt gctcatacta cattgagtag acacatttaa 1260
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ttttttttaa aaaagctcat ttcatgctct gcaaaaggag agactcccat ga agcctttt 1500
gaaaggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaacctt 1560
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cacatgggag cagtcocatg atgacagcct ctatcctaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagtgtt 1740
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aactgtttat atgtgttgaa aaccaaaatg acatcttttt aaagctttac cataaaaaaa 1860
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catttgataa tgataaaaac cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gttagaaaaa ggtcaatgct atttttgttt ttagaatcat taccctttac 2040
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cagcacttgt ctcattttaa tgtaaaagt ttgcttcatt ttccctacagg cagtctctct 2160
cttcctcaca gtccactgt gcaggtgcta ttgttactct tacgaatat tttagtaatt 2220
ttattttctt ctaagtgaat tttctagcct gcactttgat gtcattgtgt ccctttgtct 2280
ttcaaatccc aaggttcccc tgtggccctc tcctttacc tggaaggcc tcttgagac 2340
cttaccctcg gctgtttgga ctttgtatc tttaaatat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa 2416

```

<210> 382  
 <211> 378  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(378)  
 <223> 3' terminal sequence. homeo box a5 (HOXA5)  
 gene.

```

<400> 382
tttttttttt ttgttatagt tacttcaagt aacacagctt gcttcatata aataagttaa 60
aacatctatt ttttttcaag aaaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggatc cgctaataac tgctcagtac tttaaacgct cagatactca 300
ggagcgaag gccctccctt gccgcgggnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

<210> 383  
 <211> 439  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature  
 <222> (1)..(439)  
 <223> 5' terminal sequence. homeo box a5 (HOXA5)  
 gene.

<400> 383  
 aaatcaagca cacatantaa aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60  
 cgctatccaa atggcccggg ctaccagttg cataaattatg gagatcatag ttccgtganc 120  
 gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180  
 atggatctca gcgtcggcng ctcgngctcc ngcactttgg ctccggagag cgcgcccgca 240  
 gctacgtnc aagccacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300  
 acgcactctn cctcancncg atccgctgcn ctgctccgnc gtnggccccct tcgcccnnga 360  
 ancgacanna ccaangggcg gaaaaactcc cttaaggca a ctccagcngg cgctcggcg 420  
 cgacngcggg aagcaccga 439

<210> 384  
 <211> 813  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(813)  
 <223> homeo box a5 (HOXA5) gene.

<400> 384  
 atgagctctt attttgtaaa ctcatittgc ggctgctatc caaatggccc ggactaccag 60  
 ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120  
 cactccggca ggtacggcta cggctacaat ggcattggatc tcagcgctcg cgcgtcggcg 180  
 tccggccact ttggctccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcgggc 240  
 ccgcgcgagc ccaggctacag ccagccggcc acgtccacgc actctctca gcccgatccg 300  
 ctgcccctgct ccgccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360  
 tccttaagca actccagcgg cgctcggccc gacgccggca gc accccat cagcagcaga 420  
 gaggggggttg gcacggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480  
 agtgcgcaga gcgagccgag cccggcgccg cccgcccaac ccagatcta cccctggatg 540  
 cgcaagctgc acataagtca tgacaacata ggcggcccg aaggcaaaag ggcccggagc 600  
 gctacacgc gctaccagac cctggagctg gagaaggagt tccatttcaa ccgttacctg 660  
 accccagaaa ggaggattga aatagccat gctctttgcc tctccgagag acaatttaa 720  
 atctggttcc aaaaccggag aatgaagtgg aaaaagata ataagctgaa aagcatgagc 780  
 atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385  
 <211> 447  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(447)  
 <223> 3' terminal sequence. x-box binding protein  
 1 (XBP1) gene.

<400> 385

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```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca ctttcagaa 60
gtacactag caggaaaaaa ttccatcaag catttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaag gagccccctc agcaggtgtt 180
cccgttgtct acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaagtac ccttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaattct aaaagctgta gttctcaatt atagtaatat ttctacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447

```

&lt;210&gt; 386

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

&lt;223&gt; 5' terminal sequence. x -box binding protein

1 (XBPl) gene.

&lt;400&gt; 386

```

aagaacctgt agaagatgac ctctgtccgg agctggggtat ctcaaatctg ctttcatcca 60
gccactgcc aaagccatct tctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaacatc tcttgggagg 180
acacttttgc caatgaaact ttccccca gc tgattagtgt ctaagggaatg atccaatact 240
gttgcccttt tcttgacta ttacactgcc tggaggtatg cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaaga 360
ttctatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagttaa gaaatattac tnataattgg ag 462

```

&lt;210&gt; 387

&lt;211&gt; 1836

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1836)

&lt;223&gt; x-box binding protein 1 (XBPl) gene.

&lt;400&gt; 387

```

ggcgctgggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaaccgcgc cgacgggacc cctaaagtgc tgcttctgtc ggggcagccc 120
gcctccgcgc ccggagcccc ggccggccag gccctgcgc tcattggtgc agccccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgctc 240
acgcactgga gccccgagga gaaggcgctg aggaggaaac tgaaaacagc agtagcagct 300
cagatgcga gagatcgaaa gaaggctcga atgagtgcgc tggaacagca agtggtagat 360
ttagaagaaq agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggccttgtag ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctggtgtgt 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtgc 540
gcagcactca gactacgtgc acctctgcag caggtgcagg ccagttgtc acccctccag 600
aacatctccc catggattct ggcggtattg actcttcaga ttacagagtct gatattcgtg 660
tgggcattct ggacaacttg gaccagatca tgttcttcaa atgcccttcc ccagagcctg 720

```

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```

ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcctcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaa 900
ctaagtgtgt agtgaaaatc gaggaagcac ctctcagccc ctccagagaa gatcacccgt 960
aattcattgt ctcaagtgaag gaagaacctg tagaagatga cctcgttccg gagctgggta 1020
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acagtgaact tggatagcgg ggttcccttt ccccatcag tgacatgtcc ttctgtcttg 1140
gtgtaaacca ttcttgggag gacacttttg ccaatgaact ctttccccag ctgattatgt 1200
tctaaggaaat gatccaatat tgttgccttt ttcttgaact attacactgc ctggaggata 1260
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gcagtccaag gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
acagctttta agattgtact ttatctttaa aagggttgta gttttcccta aaatacttat 1500
tagtgaaggc tcattagaca aatgtcttga agtagacatg gaatttatga attggttctt 1560
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tgaagatcaa gaactctttt tgaaattata gaaatttact atgtaaat gc ttgatggaat 1740
tttttctgct tagtgtagct tctgaaaggt gctttctcca tttattttaaa actcccactg 1800
caattaaaag gtacaatgca aaaaaaaaaa aaaaaa 1836

```

&lt;210&gt; 388

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 388

```

tttttcttaa ataatttatt ttttaatggt gactcttgtg aaaagtaca tttatttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggttttcta ttagggacaa ttaaatgtgc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaaa ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttaa gagaattaga tgaaaacact 240
gaagtttatt tgngtatcct tggaaangaa ttataaagat tgccttgga aaaactt agg 300
gggctctaag gggaaagtgt tgccataatag tatgagtaaa ggctgtgtag agttatggat 360
cacaatatatt ttcaggccent aagtacagac cccnnaaatg gcagccttta tcnccgggga 420
aatgcattt ccc 433

```

&lt;210&gt; 389

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 389



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```

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc acctttttta 60
ttttattaca aacttcaaga ttattttaagt gaagatatatt ctccagctct ggggaaaaatg 120
ccacagtggt ctccctgagag aacatccctt ctttgagtca ggctgtgggc aagtctctga 180
ccacaggagg taaattingnn cctctt

```

&lt;210&gt; 390

&lt;211&gt; 4426

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein  
3 (TNFAIP3) gene.

&lt;400&gt; 390

```

tgctttgacc aggacttggg accttgcgaa aggatcgcg ggcccgagaga ggtgttggag 60
agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat ggggaaagct 120
tgaagatgac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
catttttaaaa ccattgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtctt 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccagge caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtag taggaagagg gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
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tatgatactc ggaacttgaa tgatgaatg gacaatotta tcaaaatggc ttccacagac 600
acaccatgg cccgaagtgg acttcagtag aactcactgg aagaaatata catatttgc 660
ctttgcaaca tctcagaagg gccaatcatt gtcattttcag acaaaatgct aagaagtgtg 720
gaatcaggtt ccaatttcgc ccttttgaaa gtgggtggaa tttaactgct tctccactgg 780
cctgccaggg aatgctacag ataccctatt gttctcgct atgacagcca tcattttga 840
cccttggtga ccttgaagga cagtgggcct gaaatccgag ctgttccaact t gttaacaga 900
gaccggggaa gatttgaaga cttaaaagt cactttttga cagatcctga aaatgagatg 960
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cagctttctc tcatggatgt aaaaatgtga acgcccaact gccctctctt catgtctgtg 1260
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aggagcccg gctgccctt cactagtaat gtgcagcaca a cggattttg tgaacgttgc 1560
cacacgcgc ggcaacttca cgccagccac gcccaagacc acacaaggca ctgggactcc 1620
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tgccacagag ctggaaaagca cgccctcgtc ggctgcctgt ctaagctgc acggaactcc 1860
ggggacagga cggggacgag caagtgcaga aaagccgctc gcgtgtatt ttgggactcc 1920
gaaaacaagg gcttttgcac actgtgtttc atcgagtaca gagaaaacaa acatt ttgct 1980
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gcctcctgca agaactcct ggctcgcgc agcgaggagc totgcatgga gtgtcagcat 2280
cccaaccaga ggaatgggccc tggggccac cgggtgtgac ctgccccga agaccccccc 2340
aagcagcggt gccgggcccc cgctctgtgat cattttggca atgccaagtg caacgggtac 2400

```

```

tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaacacagg tgggtcacct 2460
cctgcaagaa gtggggcctc gagctgtcag tcatcatggt gctatcctct gaaccctca 2520
gctgcacact caacagtggt cttaaagggtg tctgagcagg agaggaaaga taagctcttc 2580
gtggtgccca cgtatgctcag gtgttgtaac ccgggagtggt tcc caggtggt ccttagaaa 2640
caaaagcttgt aactggcaag ggatgatgtc agattcagcc caaggttctc cctcctctac 2700
caagcaggag gccaggaaact tctttggact tggaaagtggt gcggggactg gccgaggccc 2760
ctgcaccctg cgcatacagg ctgcttcacg gtcttggctg agaaagggaa aagacacaca 2820
agtgcggtgg gttggaga ag ccagagccat tccacctccc ctccccagc atctctcaga 2880
gatgtgaagc cagatcctca tggcagcag gcctctgca agaagctcaa ggaagctcag 2940
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cctttcctga ggaccgcgca gaaatgcaga accatccatg gactgtgatt ctgaggc tgc 3060
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&lt;210&gt; 391

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(440)

<223> 3' terminal sequence. serum response factor  
(c-fos serum response element-binding  
transcription factor) (SRF) gene.

&lt;400&gt; 391

```

ttttttgtg cacaataatg atacatttat tgaaagagta tttttttttt aatacaaaag 60
aaagctctgt acataggact gtgacctagt ccactattcc tgggtcagca tcccagggga 120
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accacacac acatacccca gagccaccga ggaagggaaa caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgcatgtcc tcccaaggcc acgtccacac 300
aacacacatt ataagcactt tgccgtattc actcaatnng gttctgtctt tgtgggaagg 360
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tgatggtgga gtgaacaag

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440

<210> 392  
 <211> 471  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(471)  
 <223> 5' terminal sequence. serum response factor  
 (c-fos serum response element-binding  
 transcription factor) (SRF) gene.

<400> 392  
 aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60  
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 agtatttatg taattttgat aggggccatg ccaacncccc tcttccccct ttgnnagna 240  
 ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300  
 accaccatata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatatt 360  
 cttaacccct aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420  
 atgggggaag attttaattgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393  
 <211> 4201  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(4201)  
 <223> serum response factor (c-fos serum response  
 element-binding transcription factor) (SRF) gene.

<400> 393  
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 g 4201

&lt;210&gt; 394

&lt;211&gt; 563

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(563)  
 <223> 3' terminal sequence. sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9) gene.

<400> 394  
 tttttaatgc aatgtatatt tattgtaac aataatatac aaaaaaaaaa aagagaaaaga 60  
 aaaagggaaa ggtaagtttc acggagagaa caaaagggtt ggggctggga gggaaacaag 120  
 tgaacaaaac aaaacacgaa caaaaaccaa agcttttacc taagacaaa atatgattta 180  
 aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatcacaga 240  
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 taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatctct 360  
 aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atcccccca 420  
 ggtagcctcc ctcaactcaa gagaagatgc ngagaaatat gggatggaca catgctcgca 480  
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 gtctntggcc gaaancctgg caa 563

<210> 395  
 <211> 3936  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(3936)  
 <223> sry (sex determining region y) -box 9  
 (campomelic dysplasia, autosomal sex -reversal)  
 (SOX9) gene.

<400> 395  
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 gtttcaaccc cggaactttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120  
 cttttgctct ttttctccc ctctctctcc tctccaattc gctccccccc acttggagcg 180  
 ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggtg gccgc cgac 240  
 gcgccagctt ccccgggagc cgttctctcc gcatacgggc agccgagggg agagagagccc 300  
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 ccggggccgc gtatgaatct cctggacccc ttcatgaaga tgaccgcaga gcaggagaag 420  
 ggccctgtcc gcgccccagc ccccaccatg tccg aggaact ccgcggggtc gccctgcgcc 480  
 tccggctccg gctcggacac cgagaacacg cgccccaggg agaacacggt cccaagggc 540  
 gagccccatg tgaagaagga gagcgaggag gacaagttcc ccgtgtgcat ccgcgagggc 600  
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 ggcatgagcg aggtgcactc ccccgcgag cactcggggc aatccccagg cccaccgacc 1080  
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 ggcagctacg gcatacagc caccggcgcc accccggcga gcgcggggca cgtgtgtagt 1380  
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&lt;210&gt; 396

&lt;211&gt; 204

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(204)

<223> 3' terminal sequence. cadherin 15,  
m-cadherin (myotubule) (CDH15) gene.

&lt;400&gt; 396

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tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgagggtcac tggaggagg caaaggaggg actaggagg 120

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251/292

tgaccgcgat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180  
ctggccgcc catccanact cagg 204

<210> 397  
<211> 458  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(458)  
<223> 5' terminal sequence. cadhe rin 15,  
m-cadherin (myotubule) (CDH15) gene.

<400> 397  
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<210> 398  
<211> 2833  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2833)  
<223> cadherin 15, m-cadherin (myotubule) (CDH15)  
gene.

<400> 398  
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ccagagaacca caagcgtctc ccctaccccc tggttcagat caagtccgac aagcagcagc 300  
tgggcagcgt catctacagc atccaggggc cggcgctgga tgaggagccc cggggcgctct 360  
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ccacggacct ggaattgta gttgtggatc agaatacaca ccggccagcc ttctgcagg 540  
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aggccacaga tgccgacgac cccgagacgg acaacgcagc gctgcgggtc tccatcctgc 660  
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tgtctgaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840  
acaatgcccc cgaattcacc agggatgagt tcttcatgga ggccatagag gccctcagcg 900  
gagtggatgt gggacgcctg gaagtggagg acagggaacct gccaggctcc ccaactctgg 960  
tgcccgaggtt caccatcctg gaaggcgacc cagatgggca gttcaccatc cgcacggacc 102 0

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```

ccaagaccac  cgaggggtgtt  ctgtccattg  tgaaggccct  ggactatgag  agctgtgtaac  1080
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tgcgtgcggg  gggcacaggc  ctacgc ctgg  gcgcactggt  catcgtctg  gccagcgccc  1920
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ggggcaagg  gctgctgcac  ggccccagg  agcactctcg  agacaatgct  ctcaactacg  2040
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aggccaggga  ggtgtttct  cctggggcac  tgcctaccag  acacagaggg  cggacagcct  2520
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gaggcagct  gaggctcacg  ggccccagcc  cctgggccc  gggggcagct  ccttctctga  2640
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tcccactctt  gccctctacc  agtgaacctc  atctttgtat  gaaagacagc  aacctcctgg  2820
gtaaatctga  atg  2833

```

&lt;210&gt; 399

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(646)

<223> 3' terminal sequence. b-cell c11/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 399

```

tatctcacac  tgtactttat  tttttctcac  aatattaact  agacagacaa  ggaagattta  60
atggcaatgt  gactttttcc  aacaacacaa  acaaagtgcc  attata gcta  atgggtggcca  120
actggagact  tacttttacc  taacctatga  aagtatcctt  accgtatttt  ttatgtgtac  180
agtgttgtag  aatatcagcc  acctcttaaa  agtatcaatc  ttaaaaagag  ccatggaagg  240
taaaagtatg  aaaaactctg  taacaaaagc  ttctaatata  aaaaacttta  ttgtacactt  300
atttttattt  aaaaacaaaa  taac cccagt  aactcaaaac  aaaagcaaac  cttggttgaa  360
aacttaagaa  ggtataataa  aaaaaccac  caaaagaaag  ctccccaaa  agaaatgcaa  420
tccactgtca  ctcttgcaaa  ttctaccttg  gagggaaaaa  cttaatgaaa  tgagctatct  480
ggagggccca  cggagatttt  ccaaaaggtt  taggtgcatg  gatttactca  gtatctacnt  540
acagtcttat  ttattaatag  ctccagantc  ctgattgagc  gagcctttcc  atctccacca  600
gtgtccccc  ttctgtgcnc  acttgggntg  cagacacctt  gtgttg  646

```



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<210> 400  
 <211> 465  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(465)  
 <223> 5' terminal sequence. b-cell cl1/lymphoma 2  
 (BCL2) gene.

<400> 400  
 ggatttttaa caataaatgt gcagttttta ctaacaggat atttaatgac aaccttctgg 60  
 ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20  
 aattaagcaa tgtgaaactg aattggagag tgataataca agtcctttag tcttaccag 180  
 tgaatcattc tgttccatgt ctttggacaa ccattgacctt ggacaatcat gaaatatgca 240  
 tctcactgga tgcaaaagaaa atcagatgga gcatgaatgg tactgtaccg gtccatctgg 300  
 actgcccag aaaaataact tcaagcaaac atcctatcaa caacaaggtt gttctgcata 360  
 ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420  
 aaaaattcga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401  
 <211> 419  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(419)  
 <223> 3' terminal sequence. ests (EST W73386)  
 gene.

<400> 401  
 gaaggtcatt ctgctgatgg gtttattgca ggagatgatg gaccaaatgg ctctgacaca 60  
 tgcacacgct cctggggcag cctgctgcgn gtnctgttcc catga ccccc agggccctct 120  
 atgcttcccc ccaggggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180  
 tctttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240  
 agaacataaa agcatcttca acattcgtca ttgagccaaa cgaacacag tgtttggtc 300  
 aagagccggc gacactngca tcc ctatcca cagtggaac ctgcccttgg gcttngttga 360  
 ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402  
 <211> 568  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(568)  
 <223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine  
esterase 3) (GZMA) gene.

```
<400> 402
tcatgcaaat tgtattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaacg 60
gttatttaaa ctgtccocctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgagggtct cgcatttat tttcaaggcc aaaggaagtgt 180
acccctcggg aaacaccctc gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttcacacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcactca 360
gagtatcggg acccaagatg cactatttgt gagtccctgc ccaccctggc aacttggcac 420
atggttctcg gntttccat caatccccc ttttagggag atgaaggata gtcacatatn 480
tggtnatttt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tggnagggga aanccttt 568
```

<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic  
t-lymphocyte-associated serine esterase 3) (GZMA)  
gene.

```
<400> 403
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcttc tctctoaagt ttctgtttctc tcttgctaatt tcttgaagat gttctgtgaaa 120
aaattattgg aggaaatgaa gtaactcttc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgctttgta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaaggtgac cttaaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaataa agggggatga tgtgaaacca ggaaccatgt 480
gccaaagtgc aggtgtgggg aggactcaca atagtgcatc ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaaatgaa atggttttgtg ctggaaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctgggaag cctttgttgtg gcgaggggtgt ttcccgaggg gtcacttcct 720
ttggccttga aataaaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accggttcct 840
ttcatttact gtggtcttct aatcttttca caaataaa 878
```

<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

```

<400> 404
gcagtgaccg tgctcttacc cagctctgct tcacagcgcc cacctgtctc cgcccctcgg 60
cccctgcgcc ggcttttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcate ctcccgtgctc agcagcgcgct ccccggccgg gataaantctt ctttattaca 180
attaatcanc g                                     191

```

```

<210> 405
<211> 245
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(245)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

```

```

<400> 405
ttttcaactt aaatgctttt attgacaatg tcttggaaaca ataagcaaac aatgctttaa 60
tttttcattc aaattcactt tcacatgtc aaaagacctc aaggtagaaa aaaataaaaat 120
aaaaataata atactgtgaga atccatctta ataaataaat taaaaacaca ataaacggtt 180
ttcatggaaa actgttaatg tcngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt                                     245

```

```

<210> 406
<211> 489
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(489)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

```

```

<400> 406
gcgncgcgct caccgaaggg ngnangtaga cagcgggtca gagccgcct agagccggag 60
gacaccccaa atacaacat accacggaga gacctgggat ctgagttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaataactt aggagacttg tt tactcag agtggaat tttgccagg acaagtgtaa 240
cacaaagaaa caaacacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtg 300
gtcccggcag tctctcccg gcactggctc gtccctgggt tctcaagggt ccatcgcgcc 360
acagcgctcg tccacctgct cagcgagacc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaatatg gcagatgcc aagtatgctt gtctgaactt 480
gaacaagac                                     489

```

```

<210> 407
<211> 247
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(247)
<223> 5' terminal sequence. interleukin enhancer
        binding factor 1 (ILF1) gene.

<400> 407
tgttttcagc ctatggaatg atttcctttt gtctgtcttg ttcagttica gacgaagcta 60
ctctggcctc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcggt ggacaggtgg acggacgctg tggccgcgat gaaccttgag 180
aaccacggga cgagccagtg ccgggaagga actgccggga ctccaccganc tgcncttaac 240
tgtttctc                                     247

<210> 408
<211> 3059
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3059)
<223> interleukin enhancer binding factor 1 (ILF1)
        gene.

<400> 408
gccccccccc cagcctcctt cccctcctcc gcgccgcgcg tgctcccgcc cctcgcgcgc 60
gtctcgtcgc tcgccggcgc gctcgcgctc gccccctccc ctacagctccg gtgcgcgcgc 120
ggcgacgacc ccgcgccttg gctcgcgcgc gccaccggcg ccgcgcgcga gcggcccgcg 180
ggccctcagc caggcccatg gcgcgcgcgc ggccgcgctct cgggccgggc accacgcggg 240
cgccggggcg ggggcgcggg gccggggggcg ggtcccgccg ggccgtgggc cgtggggcgc 300
ctggaggggc gcgagttcga gtatctgatg aagaagcgct cggtgaccat cggccccaac 360
tcgtcgcagg tcctcgttga cgtgagcatg ggccactcga gcttcactct ccggcgccac 420
ctcagatctt gacgccccc gggcggcgcg gccatggcgg ggccgctccg gagctgccgc 480
ccgcgcagcc caggcccgac gccgcgcgcg acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt gacgcggctg ttccagaggg ccgggggcgc gccgctgcag ctgccgcgcg 600
tgtgcacatt caggttcccc agcacaaaac tcaagataac gttcaactgc ctgtccagcg 660
aagaagagaga gaagcaggag cgctctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccctgcac catcaacatt ccagacacca tggcccaact catcacctc ctgcctcccc 780
ccacgggaac catcagcgct gcaaaactct gccctccag cccccgggga gcggggtctt 840
cagggtacaa ggtggggcga gtgatgccat ctgacctcaa tttaatggct gacaactcac 900
agcctgaaaa tgaaaaggaa gcttcagggt gagacagccc gaagatgat tcaagccgcg 960
cttactccta ccgcagctg atagttcagg cgattacgat ggctcccgac aaacagctca 1020
cctgaacgcg gatttataca cacatcacta aaaattatcc ctactacagg actgcgggca 1080
agggctggca gaattcaatt cgcacaaatc tctctctgaa tcgttatctt atcaaaag tgc 1140
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gcaaattaat agaacaggct ttaggaaac gacggcctag gggcggtccc tgcttttagaa 1260
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tgctgtctga cctcagtggt gccacagacc ctgagagcct gtcgagggaa ggttcgcgg 1380
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agcggcagct accacagggc atcaagcctg tcacctacac tgtggccacc ccagtgacca 1560
cctcgacctc ccagccaccc gtcgtgcaga cggttcacgt cgtccaccag atccacagg 1620
tgtcggtcac cagtgtggcc ggaactggccc cagcgaacac gtacactgtc tctggacaag 1680

```

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```

ctgtgtgtcac cccggcagcc gtgctggccc ctcttaagcc agaggccag gagaatggag 1740
accacaaggga agtcaaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcactgcccag cgggatacatt cagacggcac agaccacccc ggtccagacg gtgacacatg 1860
tacaacagggc acctctaggt caacaccagc taccataaaa aactgtaaa ccaaacggca 1920
ctcacgtggc atcagtcccc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca caagcatccg catcgccctc cctgccaca aagcgccaca 2040
acggtgacca gccggagacca cgggagctga agcggatcaa gacagaagac ggcgagggca 2100
tcgtctattgc cctgagcgtg gacacgccac cggcagccgt aaggggaaaag ggtgtccaga 2160
actagcgacc gggagagctt ttctttaacg atatcaactc tgtgtgtcca aaaggagac g 2220
cggcctcccc ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaacca aaacccagct gcccttaaca ctctttaaag acagaagtca cacttgaaca 2340
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gggggagcca tccccgccg cctcacagga ccacaccagg agcggagaca tgtggaatta 2580
gagtatattg aggtgtcctt tctttacaaa ataatggggt cttgggcatt tcacatcact 2640
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ctgatgaatt ttaaccacct ccatttcagc atgtggctcg cgtggac agg tggacggcag 2880
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ggactcacgg agctgcactt aactgtttc ttctgtgcta tttttgttg tttgtttctt 3000
tgtgttgact ttgtccctgg caaaattttc cactctgagt aaaacaagtc tcggaaattc 3059

```

&lt;210&gt; 409

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDI A) gene.

&lt;400&gt; 409

```

tttttttttt tccttcagg gcattttatt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gccctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcaattggt cctctgtttg ttcttggtcg ggtcagggaa 180
ggcctgcgcn ggggtgtggc a
201

```

&lt;210&gt; 410

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDI A) gene.

&lt;400&gt; 410

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ggcctctgct gccctttctg tgcctccacg gttctatctc cccgtcacac ccgaggcctg 60  
 gcttcaggag ggagcggana gccattctcc aggcctcggt gttgcccttg gacgtgtgctg 120  
 tctgctgtctc cggggtggan ctgggggtgtg ggatgcacgg cctcgtgggg gccgggcctg 180  
 cctccagccc cgtcgtctcc tggccagccc cc ttgctgct gtcgggtccc tctaaccatg 240  
 atgccttaac atgtggagtg tacctgtggg gctcactaa gctctaan cactgtg 297

&lt;210&gt; 411

&lt;211&gt; 1819

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha  
(ARHGDI) gene.

&lt;400&gt; 411

cctgaaccgc gcgcccgaa cctccgggtg cccgaccag gctaagcttg agcatggctg 60  
 agcaggagcc cagacccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120  
 actcgtgcaa ctacaagccc cgggcccgag agagcatcca ggagatccag gagctggaca 180  
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&lt;210&gt; 412

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

259/292

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(306)

<223> 3' terminal sequence. complement component  
4a (C4A) gene.

&lt;400&gt; 412

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 gctgcccgtc ggcggttgcn tccggcacag gcgttcagag ggcattctct cgtaccagct 240  
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 anccat 306

&lt;210&gt; 413

&lt;211&gt; 5417

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5417)

&lt;223&gt; complement component 4a (C4A) gene.

&lt;400&gt; 413

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<210> 414  
<211> 408  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(408)  
<223> 3' terminal sequence. cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 414  
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aaccttgagt ctatagtttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180  
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<210> 415  
<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 5' terminal sequence. cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 415  
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gcagaagcca aaaatatcac atggttttaa gatgggaaga tgatcggctt cctaaactgaa 120  
gataaaaaaa aatggaatct gggaagtaat gccaggacc ctcgagggat gtatcagttg 180  
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gtccttgcct ttggggtcta cttcattgct ggacaggatg gag ttcgcca gtcgagagct 360  
tcagacaagc agactctgtt gccaatgac cagctotacc agccctcaa ggatccgagg 420  
aagatgacca gtacagccac ctccaagggn aaccagt 457

<210> 416  
<211> 822  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature

262/292

&lt;222&gt; (1)..(822)

&lt;223&gt; cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

&lt;400&gt; 416

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&lt;210&gt; 417

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(439)

<223> 3' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b  
(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 417

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acatctttat tgggaagact ctgaacaacc aacctacccc c caccttcaa gtctggggaa 60
ggnaaggcag gantctgcgc cctctctcca tatgtacaat cttttccgaa tctacttga 120
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gccgccccca aaggccgct

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43 9

&lt;210&gt; 418

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(234)

<223> 5' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 418

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acgggggatg cccaacgtcc ttggggagct gaacagtctg gacccccatg gcatcgagag 60
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cccgttcttc ccgcgcgtcag cctctgtgcc agacctgac ttctctctgt ggcacctgt 180
tcctcgcccg gcnngggaggc cctggggggc ctgnacctcc tggacgatg ggtt      234
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&lt;210&gt; 419

&lt;211&gt; 2314

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral  
oncogene homolog b (nuclear factor of kappa light  
polypeptide gene enhancer in b-cells 3) (RELB)  
gene.

&lt;400&gt; 419

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&lt;210&gt; 420

&lt;211&gt; 214

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 420

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acaaagcaaa gctgcgacaa aaccgagtc catcagtaat agtatgcatc ggcaaaaggg 180
catattaatc catcaaacac aatttggtcat ttga 214

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&lt;210&gt; 421

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 421

```

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gtttagagct gtcaccctag aaaca acata ttgtcccatg agcagggtgc tgagacacag 360
accctttgc attcacagag aggtcattgg ttatagagac ttgaattaat aagtgcatt 420
atgccagttt ctgttctctc acagggtgata aacaatgctt ttgtgacct acatactctt 480
cagtgtagag ctcttgtttt atgggaaaag gctcaaatgc 520

```

&lt;210&gt; 422

&lt;211&gt; 6450

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(6450)  
 <223> estrogen receptor 1 (ESR1) gene.

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 gggagcccag gagctggcgg agggcgcttcg tccctgggagc tgcacttgct ccgttcgggtc 180  
 gcggcgcttca ccggaccgca ggctcccggg gcaggggccgg ggccagagct cgcgtgtcgg 240  
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 ggtttctgag ccttctgcc tgcggggaca cggctgtcac cctgcccgc gccacggacc 360  
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&lt;210&gt; 423

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(580)  
 <223> 3' terminal sequence. pre -b-cell leukemia  
 transcription factor 1 (PBX1) gene.

<400> 423  
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 gaggcacagg gccaggggaag atgacgaaaa ccaggctgac agctggaggc agggaaaggt 180  
 ggctttctacc cagaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240  
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 gccgacaggg tcagccggga tgcgattgtc gggagatcag ttggagttat cagagtgaac 420  
 actgccaggg ccttctgtag gggagggtcac tgatgaagg gtatgtagcat cctgccaac 480  
 tccattagca ctgattgcct gcg gactgta catctgactg gctgcgagtc catcactgta 540  
 tcctcctgtc tggtgataa catggcgaag ggtatccacc 580

<210> 424  
 <211> 503  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(503)  
 <223> 5' terminal sequence. pre -b-cell leukemia  
 transcription factor 1 (PBX1) gene.

<400> 424  
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 ttgaaataag cgaatccggt acaagaagaa cataggtaaa ttccaaggagg aagccaatat 120  
 ttaatgtgcc aaaacagctg tcaactgtac caatgtgtca gcccatggaa gccaaagctaa 180  
 ctgcgccctca actcccaact cggtgtgtgg atacccttcg ccatgtttac agccagacag 240  
 gaggatacac tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300  
 tggagggttg caggatgcta ctacccttc atcagtgacc t ccctacag aaggccctgg 360  
 cagtgttac tctgatacct ccaactgac tcccagcaat cgcaccccg ctagccctgt 420  
 gccccagttg gccaggggca ggaggagggt ttctctccc aacgtgtaag cggtcagact 480  
 ggaggtcaaa cgattaggca aac 503

<210> 425  
 <211> 1819  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1819)  
 <223> pre-b-cell leukemia transcription factor 1  
 (PBX1) gene.

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<400> 425
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gagatggagc agcagcccag gctgatgcac tcccatgctg ggtcgggatg gccggagcac 180
cccggcctgt ccagcacctt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcagacat ttggagacat ttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgagg ccagaaaaaca tgcctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
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<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli -kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)  
(GLI3) gene.

<400> 426

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cacatctcag ttagggtgaga tgagattgct aaaatacata cagaactaaa aaaaacagcca 180
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atctggtacc ctccagggcc aggtcg 506

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<210> 427  
 <211> 239  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(239)  
 <223> 5' terminal sequence. gli-kruppel family  
 member gli3 (greig cephalopolysyndactyly syndr ome)  
 (GLI3) gene.

<400> 427  
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 tgtctctatt taataaaacaa aaagcctggg gtgggtgggc atgcctgtag tctcagcctc 120  
 ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180  
 agagacaggg ttaccacag ttgccaggg cagtcttgaa ctctgagcc caagtgatc 239

<210> 428  
 <211> 5054  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(5054)  
 <223> gli-kruppel family member gli3 (greig  
 cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428  
 cgatactagc tgggcatttt tggctgaaga gagctgaagt aatgagaaga catcatggag 60  
 gccagtgccc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120  
 tgcctcactc gaacagatgt gagcgagaaa gccgttgcc tccagcaccac ttctaatgag 180  
 gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240  
 cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300  
 gccctattga tcaagaaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360  
 ccgtaccgcg ggaagggtg tt tgccatggac cccaggaatg gttacatgga gccccactac 420  
 caccctctct atcttttccc tgccttccat cctctctgtac caattgatgc cagacatcat 480  
 gaggcgctt accattacga tccatctccg attctctc  
  
 cat tgcatatgac ttccgcctta 540  
 tctagttagc ctacgtatcc ggacctgccc ttcattagga tctcccaca ccggaacc cc 600  
 gctgtgcttt ccgagttccc cttcagccct ccacatccct acattaatcc ctacatggac 660  
 tatatccgct ccttgccacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720  
 agccctacag atgcgcccc tgcaggagtc agcccagcag aatactatca tcagatggcc 780  
 ctgctaactg gccagcgcag cccctatgca gacatt attc cctcagctgc caccgcggcg 840  
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 attctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200  
 cctggcccaa cttttccaac acagaggcct attccaggga tccctaeggt tc tgaacccc 1260

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aacgaccata	ttcatggaga	gaagaaggag	ttcgtgtgca	ggtggctgga	ctgctcaaga	1620
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ttctatgacc	aaacccgtgg	cttcagtcag	caagacacga	aagctgtgtc	attctctatt	4440
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ggtgctaate	aggtgacaag	acacagtgag	agcctcgaca	gccatgacct	ggaaggggta	4560
cagattgact	tgatgcatc	catagacgat	ggggacacct	ccagcctgat	gtcgggggcc	4620
ctgagcccaa	gtatcatcca	gaacctttcc	catagctcct	cccgccctac	cagcgctcag	4680
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gatgtgtttc aattatatc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980  
 agggagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040  
 tttttaaaaa aaaa 5054

&lt;210&gt; 429

&lt;211&gt; 271

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(271)

<223> 3' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

&lt;400&gt; 429

aggagacttg ttttactcag agtggaaaaat ttgcccaggg acaaagtc aa cacaaagaaa 60  
 caaacacaac aaaatagcca gaaagagAAC agttaagtgc agctcggtag gtcccggcag 120  
 ttccctcccg gcactggctc gtccctgggt tctcaaggtt ccatgcggcc acagcggtccg 180  
 tccactgtc cagcggagcc acatgctgaa atggagggtg ataaaaattca tcaggcgagct 240  
 gctgtaacac ggaaatgtgc agatgcc aga g 271

&lt;210&gt; 430

&lt;211&gt; 193

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(193)

<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,  
sw|Q08999|RBL2\_HUMAN.

&lt;400&gt; 430

TGCTACATT TNCCACATA AAAATGAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60  
 TTACTTNAGC NAAAGTCCCT CAAAGNGACT GAGCGNANTT AATAGTNGA TACGCATAGG 120  
 NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNINGNNGAT GGCNGTGAAT NCACTGCAAA 180  
 NAGCATTTGC CCN 193

&lt;210&gt; 431

&lt;211&gt; 184

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(184)

&lt;223&gt; 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431  
 AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60  
 ATAAGAAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120  
 AATCATTGA TTTATCGCAT CTACACATGA CCGAGAGGGG GACAAGAAAT CTCTAAGTTT 180  
 TCTG 184

<210> 432  
 <211> 242  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(242)  
 <223> 5' terminal sequence. Similar to NM\_022641 Homo sapiens chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432  
 ATTCCGGCAG ATGACTGGCC AGGGTATAAA AAGGGCCAC AAGAGACCGG CTCTAGGATC 60  
 CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120  
 TCAGGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180  
 AANAAGCTNG TGCNCTCAA ANCGTCCGT TATCCAGGT TTTTGACCAC GCTATGCTNC 240  
 AA 242

<210> 433  
 <211> 329  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(329)  
 <223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433  
 AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGG CCCAGGNAAA 60  
 CTGTGCACGAC GCCTGCCAGG GNATTTCTGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120  
 CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180  
 TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240  
 AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300  
 GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434  
 <211> 247  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature

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<222> (1)..(247)
<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434
AAATATACT GAANNNTTA AGTACAGTNT AAAACAGGST TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTGCTATAA ATATGCTGAA GCCTAGTTGT TCAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                     247

<210> 435
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(63)
<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGSAG CTGCTGTGGC 60
TTT                                     63

<210> 436
<211> 190
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(190)
<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGAG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                     190

<210> 437
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTIN TTGCACCTGC 60  
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120  
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GSAGTTTTTA CA AACGCTGC ATTTGACCOG AGTCCTTAAG AGACCTGTCC 60  
TTTCTCTGTT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120  
TACACTGGAC TTAACATATA TGCACTTGTCT GCAGGTTTCC ATAAACACCC ATGANTCAA 180  
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240  
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAATTC TCAACCTACC ACCCCTTCCT 300  
TGCCACCTC TTCTCTTCTT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360  
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420  
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTNAANAT TGGNCTTTGG GNCATTAGAG GGACAGTGAC 60  
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120  
GCCTTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCCTC 180  
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240  
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCTNNA ATCAAAAANT AAAGAGGTNT 300  
TTCNATTICT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTGGNNCAC 360  
TGGTATTTC AATAACAGGT GAGNNAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(337)

&lt;223&gt; 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 440

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AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGSCCAAC CCCCCATTCT CCACGTGGAT 180
CCTCTTCCTT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTTC TTGA GCTGCAGCTG GCGGTAGGG CNCGGGGCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCA CAGGNGT 337

```

&lt;210&gt; 441

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:prim er

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(104)

&lt;223&gt; 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 441

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TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGNAAN AGTTTNTGAA NCACCAGAAA CCTT 104

```

&lt;210&gt; 442

&lt;211&gt; 223

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(223)

&lt;223&gt; 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

&lt;400&gt; 442

```

AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCCTCCTG GCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTCCGTCT G GG 223

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&lt;210&gt; 443

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<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
      (Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
cagggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tctctgtcc 180
cttcccagan aacctaccag ggcagctacg gtttcctgt ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
      oncogene homolog 2 (neuro/glioblastoma derived
      oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac ccagccctc tacagcggta cagtgaaggac 60
ccacacgtac cctgcctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatggt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgaact gctggtgcc ctctggaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt ggggggt gccgtgggag aaccccagat 300
atgacaccc caggggaggg agcttgccct tcagcccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

```



<220>  
<221> misc\_feature  
<222> (1)..(309)  
<223> zinc finger protein 144 (Mel-18) (ZNF144) gene.

<400> 445  
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60  
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tcctatggcct 120  
caagttaagg ggggcacggg agcgccnttg acagtcatct tgcgccccct gctggtnгаа 180  
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240  
ntcgaagggg ganttgggna ngtaggggtng gtngcttgan gcccatngga actnggaaaa 300  
ccatnggat 309

<210> 446  
<211> 268  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 446  
attatcttgt gaatctactt agaaaaacac acacaagcaa tggtcacaac tataaattta 60  
aaccttttgc actaaaaaaa cacaaaaacaa caaacacaaan accacaggca tgaactgtaa 120  
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtatatttc 180  
tccttggcaa ctgtaatgtt ttngcacggg ntgatctccc gengggggta ctagtaaatga 240  
ctggctgccc gtgtagggag atgcttcc 268

<210> 447  
<211> 169  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> 5' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 447

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```

gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat ctctctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgnccct gccctactt 169

```

<210> 448  
 <211> 393  
 <212> ADN  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(393)  
 <223> 3' terminal sequence.

<220>  
 <221> misc\_feature  
 <222> (1)..(393)  
 <223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

```

<400> 448
aagtaattaa gggtagttaa attattttaa gtatacaaa tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggttaaggga gagggccaca agggaacctt ggagtgtgaa 120
agacaaggga aacacatgac atcaaagtgc aggctagaaa ttctacttag aagaaaaataa 180
cattactgaa aatattctga agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgcgt 300
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

```

<210> 449  
 <211> 217  
 <212> ADN  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(217)  
 <223> 5' terminal sequence.

<220>  
 <221> misc\_feature  
 <222> (1)..(217)  
 <223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

```

<400> 449
ttaccntggt atctctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60
tcctgnetca cctttgtctc agctaaatgt agccgcaccc gggacacagt ttgtgccaca 120
tgtgccaga attctacaa cgagc actgg aactacctga ccactctgcca nctgtgccgc 180
ccctgtgacc cagtgtatgg cctcgnetga gantgcc 217

```

<210> 450  
 <211> 157  
 <212> ADN

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; (POU2F2) gene.

&lt;400&gt; 450

```
nattcggcaa cgnaggaaagg aaagaaacta accaacaataa gagaaacaa aaaaataatc 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gacccaaaaa acaacca                               157
```

&lt;210&gt; 451

&lt;211&gt; 282

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

&lt;223&gt; 5' terminal sequence.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

<223> caspase 4, apoptosis-related cysteine protease  
(CASP4) (ex CASP1)

&lt;400&gt; 451

```
gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtcct ctgacagcac attcttggtg ctcatgtctc atggcatcct ggagggaate 120
tgcggaactg tgcattgatga gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

&lt;210&gt; 452

&lt;211&gt; 424

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(424)

&lt;223&gt; 5' terminal sequence

```

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtataaa accttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgctt 120
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggtccttc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggcgtgatgc aatttncgtg gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaagggtg gatgggcccc agcnacagct ttgnaccc ga gggcctnttg 420
gtca                                     424

```

```

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

```

```

<220>
<221> misc_feature
<222> (1)..(435)
<223> Itegin, beta 2 (antigen CD18 (p95), lymphocyte
      function-associated antigen 1; macrophage antigen
      1 (mac-1) beta subunit) (ITGB2)

```

```

<400> 453
aggagtgcgc cggctgcccc tcacctgtg gcaagtacat ctccctgcgc gagtgcctga 60
agttcgaaaaa gggccctntt ggaagaactg cagcgcggcg tgtcggggcc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc 180
ctacacgctg gaggcagcag acgggatgga cgcgtacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatgcgcgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg catctcctcg ctggtcatct ggggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtgc cagtnngaac aatgattatt 420
ccctttttca agage                                     435

```

```

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(544)

```

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&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha  
isoform (PPP1CA) (ex MGST1)

&lt;400&gt; 454

```

gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgn aagcagnacg 60
nctnacaaca tcaaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgncgtgcc acggaggcct gttccccga 180
cctgncagtt ctatggnagc agattcggcg ggaatcatgc gccacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgacctga caaggacgtg cagggctggg 300
cgagaaacga ccgtgggcgt ctcttttac c ttggagccg aggtggtggc caagtctctc 360
cacaagcacg acttggaact catctgccga gcacaccag ttgtagaaga cggctacag 420
ttctttgcc aagcgcantt ggtgacact ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544

```

&lt;210&gt; 455

&lt;211&gt; 344

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic  
subunit, alpha isoform (PPP2CA)

&lt;400&gt; 455

```

actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cacgaggaaac 60
cggcgcgggc gntgtcgngt aggcccggtg n gcggtgncgg cgcggggagga gccgggannc 120
gccggcnggg gcgggnggca ncanggacga gaagngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagnc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaagaanc caacngcaa gaggnncgan gnccagannac 30 0
ngnccngga gangngcang ggcaannnca ngaacccatg gaac 344

```

&lt;210&gt; 456

&lt;211&gt; 514

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(514)

&lt;223&gt; 5' terminal sequence

```

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
      (S100A11)

<400> 456
cagcctcccg cgctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtcctcg attgctgtct tccagaagta tgctggaa ag gatggttata 120
actacactct ctccaagaca gagtccctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatgggtca gctagatttc tcagaatttc ttaatctgat tgggtggccta gctatgggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccttt 360
gggcccctggg cctttcaaac ccaccacctn ttcttttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480
attagttatt aaagгнаatg tnaatttttt ttaa
                                         514

```

```

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
      T-lymphocyte-associated serine esterase 3) (GZMA)

```

```

<400> 457
gctggagctc atcaacaagc attcattcaa caacttcgc ctgcgagtgg ggttgaacca 60
tggacccgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtga 180
tgaggagaca gcatggggcc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcacaagg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tntaag aacctnaat 359

```

```

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

```

```

<220>

```

<221> misc\_feature  
 <222> (1)..(1251)  
 <223> endothelin 1 (EDN1)

<400> 458  
 ggagctgttt acccccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60  
 aagtgcagacg cgctctgtca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtcgc 120  
 agctctccac caccgcgcgct tgcgcctgca gacgtccgcg tcgctgcctt ctctcctggc 180  
 aggcgctgcc ttttctcccc gttaaagggc acttggggctg aaggatcgct ttgagatctg 240  
 aggaaccgcg agcgcttttg gggacctgaa gctgttttct tctgttttcc ttgggttcca 300  
 gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgcct catgattttc 360  
 tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagctcttagg cgctgagctc 420  
 agcgcggtgg gtgagaacgg cggggagaaa ccactccca gtccaccctg gcgctctcgc 480  
 cggtccaagc gctgtcctcg ctgcctccctg atggataaag agtgtgtcta ctcttgccac 540  
 ctggacatca ttgggtgcaa cactcccgag caggttgttc cgtatggact tggaaagccct 600  
 aggtccaaga gaggccttga gaatttactt cccacaaagg caacagaccg tgagaataga 660  
 tgccaatgtg ctagccaaaa agacaagaag tgcgtggaatt ttgtccaagc aggaaaaaaa 720  
 ctcagggtcg aagacattat ggagaagac tggaaataatc ataagaaagg aaaagactgt 780  
 tccaagcttg ggaaaaaagt tattttatcag cag ttagtga gaggaagaaa aatcagaaga 840  
 agttcagagg aacacctaa gacaaaccagg tcggagacca tgagaaacag cgtcaaatca 900  
 tcttttcatg atcccaagct gaaaggcaag ccctccagag agcggttatgt gaccaccaac 960  
 cgagcacatt ggtgacagac ttccggggcct gtctgaagcc atagcctcca cggagagccc 1020  
 ttgtggccgac tctgcactct ccaccctggc tgggatcaga gcaggagcat cctctgctg 1080  
 ttctgtactg gcaaaaggac agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140  
 tcccccaacc atcttctactg gcttccatca gtggttaactg ctttggctc ttctttcatc 1200  
 tggggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251

<210> 459  
 <211> 2145  
 <212> ADN  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(2145)  
 <223> 3' terminal séquence

<220>  
 <221> misc\_feature  
 <222> (1)..(2145)  
 <223> Protein tyrosine phosphatase, non -receptor type 6  
 (PTFN6)

<400> 459  
 cggcagaact gggaccacgg ggggtgtgga ggcggcccg cactgggagc tgcactgtg 60  
 gcttagtccc tgaagctctct gctgcccag actagctgca cctctcatt cctcgcgccc 120  
 ccttctctctc cggaa gcccc caggatgggt aggtgtgttc accgagacct cagtgggctg 180  
 gatgcagaga cctgtctcaa gggccgaggt gtccacggta gcttctggc tggcccaagt 240  
 cgcaagaacc aggggtgact ctgcctctcc gtcagggtgg gggatcaagt gacccatatt 300  
 cggatccaga actcagggga ttctatgac ctgtatggag gggagaagt t tgcgactctg 360  
 acagagctgg tggagtacta cactcagcag cagggtgtgg tgcaggaccg cgacggcacc 420  
 atcatccacc tcaagtacc gctgaactgc tccgatccca ctagtgaag gtggatccat 480  
 ggcacatgt ctggcgggca ggcagagacg ctgctgcagg ccaaggcgca gccctggagc 540  
 ttctcattgt gtgaga gcct cagccagcct ggagacttcg tgccttctgt gctcagtgac 600  
 cagcccaagg ctggcccagg ctccccgctc agggtaacce acatcaaggt catgtgcgag 660  
 ggtggacgct acacagtggg tggtttgag accttcgaca gctcagga cctgggtggg 720

```

catttcaaga agacggggat tgaggaggcc tcaggcgccct ttgtctacct gcggcagccg 780
tactatgcca cgagggtgaa tgccgctgac attgagaacc gagtgttgga actgaacaag 840
aagcaggagt ccgaggatgc agccaaggct ggcttctggg aggagtttga gagtttgcag 900
aagcaggagg tgaagaacct gcaccagcgt ctggaagggc aacggccaga gaacaaggcg 960
aagaaccgct acaagaa cat tctccctttt gaccacagcc gagtgtacct gcagggacgg 1020
gcagatcaaca tcccggggtc cgactacatc aatgccaact acatcaagaa ccagctgcta 1080
ggccctgatg agaagcgtaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacctct gccagatggc gtggcaggag aacagccgtg tcatcgctcat gaccacccga 1200
gagggtggaga aaggccggaa caaatgctgc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggcccga ccatgggggtc cccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcacg caggggcccat catcgtgcac 1500
tgacgcgcgc gcatcgccgc cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atggtgcgg 1620
gcgcagcgct cgggcatggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gccagttca ttgaaccac taagaagaag ctggaggtcc gtcagtcgca gaaggccag 1740
gagtcggagt acgggaacat cacctatccc ccagccatga agaatgcccc tgccaaggcc 1800
tcccgcacct gctccaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtc gcagacaagg agaagagcaa gggttccctc 1920
aagaggaaat gagcgggtgt gtcctcaggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gccccattct tt tghtaatt 2040
aaatggctgc atcccccca cctctccctg acctgtata tagccagcc agggcccaag 2100
cagggccaac cctctcctc ttgtaataa agccctggga tcaact 2145

```

&lt;210&gt; 460

&lt;211&gt; 2149

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

&lt;400&gt; 460

```

gacctgcaaa cacacacaca cacacacaca cacacacaca cacacacaca catacacacg 60
cacaggggca gccgagagac ctccctcccg cccctcccat gcccgctccc ctccctccgc 120
cgccgcgcgc gccgcgcaga tctgggacgg gccgattctg cacctccgtc cggcgctgcc 180
ctttgattcg gatttccatc ttgcattctc cggctgatcg cgggacctgg ct cgtgcaga 240
ggaggggggc cgatcgctat ggagtatttc atggtgccca ctcaagaagt gccctctttg 300
caacatttca ggaaaacaga gaaagaagtg ataggagggc tctgtagcct tgccaacctt 360
ccactaacc cagagactca gggggaccag gagcggcgga ttgcggcgga gatgcgcaac 420
agcaaccgag gtagacgcat gcagagcatc aacgcgggat tccagtcctt caagaccctc 480
atccccacca cagacgggaga gaagctcagc aaggcagcca ttctccagca gacagccgag 540
tacctcttct cctcgaggca ggagaagacc aggcctcttc agcagaacac acagctcaag 600
cgcttctacc aggagctgag cggctcgtcc cccaagcgac cgggggcaga gga caaggac 660
gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcgcgaca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtgcgct cgtcggaggc ccacatgtac ccggaaaagc tcaagggtgat tgcgcgacag 840

```



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```

gtgcagctgc agcagcagca ggaacaggtg aggctgctgc accaggagaa gctggagcgg 900
gaacacagc agctgcccgc ccagctctct cccctcccg ccccccacca ccaccccacg 960
gtgatctgtc cagcacccgc tcctcctccc tcccaccaca tcaatgtcgt caccatggcg 1020
ccctcctcgg tcatacactc tgtttccaca tcccggcaca atctggacac cato gtgcag 1080
gcaatccagc acatcgaggc caccacaggaa aagcaggagc tggaggagga gcagcggcga 1140
gctgtcatcg tgaagcctgt ccgcagctgc ccggaggccc ccacctctga caccgcctcc 1200
gactccagg cctcagacag tgacgccatg gaccagagcc gggaggagcc gtcgggggac 1260
ggggagcttc cctgactacc cccccagccc tcctctccct tctggggggc ggaggggagc 1320
ggggcagcca caggggagaa catgggcgaa tgagtgaaga attttacaa aattacgatg 1380
tcatttgggt ctcttttatg acctcttttt caatactgta aatcgacctt tgaacgaagc 1440
cactcaaccc gaggtcccgg ggctggggtg tcgcagagct gtggggagcat cgga cccca 1500
gggcggggcc tcggccccgg ggctgggagg aagctgacac ggagatgcct ggctctctc 1560
tgccaaaaag catTTTTTcc tttaaatatg ttttttaaga acagggaaaa ttaacaaaaa 1620
ccccaggtta tttcttccct gccagagcc agcctgggat tgtcagcctt caatccccct 1680
tccttctctc ttttgggttt tc tcttttct ctttaagca cttacatggt tgggggtaag 1740
actaggtctg ggcattctgg gggcccgagg gtctccgttg cttcttggtt ggggtttgct 1800
gctgctgtgc cccctccccc cttcccctc tcggcactag tctccaccc 1860
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&lt;210&gt; 461

&lt;211&gt; 6478

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; Cyclin D2 (CCND2)

&lt;400&gt; 461

```

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&lt;210&gt; 462

&lt;211&gt; 3490

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; Junction plakoglobin (JUP)

&lt;400&gt; 462

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&lt;210&gt; 463

&lt;211&gt; 1355

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
      (GADD45A)

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acctacaata aactggtagt aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
      in (NME1)

<400> 464
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ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaagga 180
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cacggaagac tggctgcag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960
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tccaggctcc cggaacgtcc ctgactctgg nttttgncct nctctnaactg ccttggnntn 180  
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(74) Agents: BREESE, Pierre et al.; Breese-Majerowicz, 3,  
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GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, PI, PL, PT, RO, RU, SD, SE, SG, SI,  
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU,  
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European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,  
GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent  
(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,  
NE, SN, TD, TG).(71) Applicants (for all designated States except US): IPSO-  
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— with international search report

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28 August 2003For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE  
GENES(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library  
including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in  
tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth  
in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate  
tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

WO 02/046467 A3

## INTERNATIONAL SEARCH REPORT

Int. Application No.  
PCT/IB 01/02811A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C07K14/47 C1201/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C120

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, BIOSIS, MEDLINE, EPO-Internal, WPI Data, EMBASE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BERTUCCI F ET AL: "EXPRESSION SCANNING OF AN ARRAY OF GROWTH CONTROL GENES IN HUMAN TUMOR CELL LINES" ONCOGENE, BASINGSTOKE, HANTS, GB, vol. 18, no. 26, 1999, pages 3905-3912, XP000979482 ISSN: 0950-9232 the whole document	1-42
X	PEROU C M ET AL: "Molecular portraits of human breast tumours." NATURE. ENGLAND 17 AUG 2000, vol. 406, no. 6797, 17 August 2000 (2000-08-17), pages 747-752, XP002235791 ISSN: 0028-0836 the whole document	1-42

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

## \* Special categories of cited documents:

\*A\* document defining the general state of the art which is not considered to be of particular relevance

\*E\* earlier document but published on or after the international filing date

\*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

\*O\* document referring to an oral disclosure, use, exhibition or other means

\*P\* document published prior to the international filing date but later than the priority date claimed

\*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

\*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

\*G\* document member of the same patent family

Date of the actual completion of the international search

25 March 2003

Date of mailing of the international search report

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Name and mailing address of the ISA  
European Patent Office, P.B. 5818 Patentlaan 2  
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Authorized officer

Luzzatto, E

## INTERNATIONAL SEARCH REPORT

Int l Application No

PCI/1B 01/02811

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HOCH R V ET AL: "GATA-3 is expressed in association with estrogen receptor in breast cancer." INTERNATIONAL JOURNAL OF CANCER. JOURNAL INTERNATIONAL DU CANCER. UNITED STATES 20 APR 1999, vol. 84, no. 2, 20 April 1999 (1999-04-20), pages 122-128, XP001146467 ISSN: 0020-7136	1-5,8,9, 12,13, 16,17, 20,21, 24-42
Y	the whole document	6,7,10, 11,14, 15,18, 19,22,23
Y	----- DATABASE MEDLINE 'Online! US NATIONAL LIBRARY OF MEDICINE (NLM), BETHESDA, MD, US; July 1997 (1997-07) SHAW-BRUHA C M ET AL: "Expression of the prolactin gene in normal and neoplastic human breast tissues and human mammary cell lines: promoter usage and alternative mRNA splicing." Database accession no. NLM9266104 XP002235792 abstract & BREAST CANCER RESEARCH AND TREATMENT. NETHERLANDS JUL 1997, vol. 44, no. 3, July 1997 (1997-07), pages 243-253, ISSN: 0167-6806	6,7
Y	----- GRAHAM J D ET AL: "Regulation of the expression and activity by progestins of a member of the SOX gene family of transcriptional modulators." JOURNAL OF MOLECULAR ENDOCRINOLOGY. ENGLAND JUN 1999, vol. 22, no. 3, June 1999 (1999-06), pages 295-304, XP000995364 ISSN: 0952-5041 the whole document	10,11, 14,15, 18,19
Y	----- MAGUIRE T M ET AL: "High levels of cathepsin B predict poor outcome in patients with breast cancer." INTERNATIONAL JOURNAL OF BIOLOGICAL MARKERS, vol. 13, no. 3, July 1998 (1998-07), pages 139-144, XP001118861 ISSN: 0393-6155 abstract	22,23

-/-

## INTERNATIONAL SEARCH REPORT

 Int. Application No.  
 PCT/IB 01/02811

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MATHOULIN-PORTIER M P ET AL: "Prognostic value of simultaneous expression of p21 and mdm2 in breast carcinomas treated by adjuvant chemotherapy with antracyclin." ONCOLOGY REPORTS. GREECE 2000 MAY-JUN, vol. 7, no. 3, May 2000 (2000-05), pages 675-680, XP009007614 ISSN: 1021-335X the whole document ---	1-42
A	FAIRCHILD C R ET AL: "ISOLATION OF AMPLIFIED AND OVEREXPRESSED DNA SEQUENCES FROM ADRIAMYCIN-RESISTANT HUMAN BREAST CANCER CELLS" CANCER RESEARCH, vol. 47, no. 19, 1987, pages 5141-5148, XP009006931 ISSN: 0008-5472 the whole document ---	1-42
A	VARGAS-ROIG L M ET AL: "c-erbB-2 (HER-2/neu) protein and drug resistance in breast cancer patients treated with induction chemotherapy." INTERNATIONAL JOURNAL OF CANCER. JOURNAL INTERNATIONAL DU CANCER. UNITED STATES 20 APR 1999, vol. 84, no. 2, 20 April 1999 (1999-04-20), pages 129-134, XP002235684 ISSN: 0020-7136 the whole document ---	1-42
A	PENALT-LLORCA F ET AL: "Expression of FGF and FGF receptor genes in human breast cancer." INTERNATIONAL JOURNAL OF CANCER. JOURNAL INTERNATIONAL DU CANCER. UNITED STATES 10 APR 1995, vol. 61, no. 2, 10 April 1995 (1995-04-10), pages 170-176, XP009007615 ISSN: 0020-7136 the whole document ---	1-42

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## INTERNATIONAL SEARCH REPORT

Int. Application No.

PCT/IB 01/02811

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE EBI 'Online! Homo sapiens cathepsin B mRNA, complete cds., 20 May 1993 (1993-05-20) CAO L. ET AL.: Database accession no. L16510 XP002235958 abstract &amp; CAO L. ET AL.: "Human gastric adenocarcinoma cathepsin B: isolation and sequencing of full-length cDNAs and polymorphism of the gene" GENE, vol. 139, no. 2, 1994, pages 163-169, ---</p>	22,23
A	<p>CAFFO O ET AL: "Prognostic value of p21(WAF1) and p53 expression in breast carcinoma: an immunohistochemical study in 261 patients with long-term follow-up." CLINICAL CANCER RESEARCH: AN OFFICIAL JOURNAL OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH. UNITED STATES SEP 1996, vol. 2, no. 9, September 1996 (1996-09), pages 1591-1599, XP001121315 ISSN: 1078-0432 the whole document ---</p>	1-42
T	<p>BERTUCCI FRANÇOIS ET AL: "Gene expression profiles of poor-prognosis primary breast cancer correlate with survival." HUMAN MOLECULAR GENETICS. ENGLAND 15 APR 2002, vol. 11, no. 8, 15 April 2002 (2002-04-15), pages 863-872, XP001146244 ISSN: 0964-6906 -----</p>	

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

# INTERNATIONAL SEARCH REPORT

ational application No.  
PCT/IB 01/02811

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☒ Claims Nos.: 6,7,10,11,14,15,18,19,22-26,28-43 (all partly)  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-43 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-43 (all partially)

Polynucleotide libraries comprising any of SEQ IDs 76-78, which according to table 10 of the application correspond to the GATA-3 gene, method for detecting cancer correlated differentially expressed polynucleotide sequences or for screening an anti-tumour agent, comprising the step of reacting a polynucleotide sample from a patient with a probe comprising any of SEQ IDs 76-78.

2. Claims: 1-3, 8-11, 16-27,29,31-43 (all partially)

Polynucleotide libraries comprising any of SEQ IDs 354-355, which according to table 10 of the application correspond to the MYB gene, method for detecting cancer correlated differentially expressed polynucleotide sequences or for screening an anti-tumour agent, comprising the step of reacting a polynucleotide sample from a patient with a probe comprising any of SEQ IDs 354-355.

3. Claims: 1-3, 8-13,27,29,30,33-43 (partially)

Polynucleotide libraries comprising any of SEQ IDs 322-323, which according to table 10 of the application correspond to the KIAA1075 gene, method for detecting cancer correlated differentially expressed polynucleotide sequences or for screening an anti-tumour agent, comprising the step of reacting a polynucleotide sample from a patient with a probe comprising any of SEQ IDs 322-323.

Inventions 4-171: subject as in inventions 1-3, however the SEQ IDs are those corresponding to genes 4-171 as listed in table 10.

As to the claims related to each of inventions 4-171, the ISA wishes to draw the applicant's attention to the following:

In view of the number of genes and sequences to which the claims relate, and of the fact that the vast majority of SEQ IDs are mentioned only in some claims and not in others, it becomes unduly burdensome for the ISA to provide for each invention the indication as to which claims are related to it. Should any additional search fees be paid, the clear definition of each invention by means of the SEQ IDs will allow the unambiguous definition of the claims that belong to the invention to be searched.



## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 6,7,10,11,14,15,18,19,22-26,28-43 (all partly)

The present remarks apply to the only invention searched, i.e. invention 1 (see "Invitation to pay additional fees"). Should further search fees be paid, similar remarks could apply to the further inventions to be searched, leading to an incomplete search also with respect to these inventions.

1) The application relates to genes which are differentially expressed in breast tumour cells compared to normal breast cells (see p. 21, 1. 15-p. 22, 1. 12). No other cells are analysed for differential gene expression of tumor vs. normal cells. However, claims 33-40 and 42-43 encompass the detection of differentially expressed sequences correlated with "a cancer", i.e. they are not limited to breast cancer. Hence, they lack support (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible.

Claims 33-40 and 42-43 have therefore been searched only insofar as related to breast cancer.

2) Claims 6,10,14,18,22 relate to a very large number of combinations comprising the GATA-3 gene related sequences and at least one other of the second group of sequences to which the said claims relate. They therefore lack conciseness (Art. 6 PCT) to such an extent as to render impossible a meaningful search covering all the said combinations. The search has thus been limited to combinations comprising the GATA-3 related sequences of set 32 (consisting of SEQ IDs 76-78) and those of sets 38, 11 and 14 (SEQ IDs 91-93, 22-24 and 30-31 respectively), these being the first sets mentioned in the various claims in the context of combinations with the GATA-3 gene.

The same applies to claims 7,11,15,19,23-26,28-43 insofar as dependent on the said claims.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.